

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
SEQUENCE LISTING

<110> Genentech, Inc.  
Ashkenazi, Avi  
Botstein, David  
Desnoyers, Luc  
Eaton, Dan L.  
Ferrara, Napoleone  
Filvaroff, Ellen  
Fong, Sherman  
Gao, Wei-Qiang  
Gerber, Hanspeter  
Gerritsen, Mary E.  
Goddard, A.  
Godowski, Paul J.  
Grimaldi, Christopher J.  
Gurney, Austin L.  
Hillan, Kenneth, J.  
Kljasin, Ivar J.  
Mather, Jennie P.  
Pan, James  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Stewart, Timothy A.  
Tumas, Daniel  
Williams, P. Mickey  
Wood, William, I.

<120> Secreted and Transmembrane Polypeptides and Nucleic  
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&lt;151&gt; 2000-01-05

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Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala  
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Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys  
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Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu  
165 170 175  
Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr  
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His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly  
195 200 205  
Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp  
210 215 220  
Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro  
225 230 235 240  
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Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly  
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Page 3

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295

300

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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 50           55           60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
 65           70           75           80

Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
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Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
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His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
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Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu
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Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
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Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
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Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His
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Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys
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Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
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His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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&lt;212&gt; DNA

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 35 40 45  
 Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu  
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 Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr  
 65 70 75 80  
 Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro  
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 Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln  
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 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 14  
 ttcgaggcct ctgagaagtg gccc 24

<210> 15  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 15  
 ggcggtatct ctctggcctc cc 22

<210> 16  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 16  
 ttctccacag cagctgtggc atccgatcgt gtctcaatcc attctctggg 50

<210> 17  
 <211> 960  
 <212> DNA  
 <213> Homo sapiens

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 17

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gggggagcag tgctggaccg cgcgcattccg cgcagttggc ctctgaccg tcatcagcaa 180
aggctgcagc ttgaactgcg tggatgactc acaggactac tacgtgggca agaagaacat 240
cacgtgctgt gacaccgact tgtgcaacgc cagcggggcc catgccctgc agccggctgc 300
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ccgtggtgtc ccccgacccc agcaggggac aggcactcag gagggcccag taaaggctga 780
gatgaagtgg actgagtaga actggaggac aagagtcgac gtgagttcct gggagtctcc 840
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aatggcagcc tgagcacagc gtaggcctt aataaacacc tgttgataa gccaaaaaaa 960

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<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

<400> 18

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Met Thr His Arg Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val
 1          5          10          15

Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu
          20          25          30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp
 35          40          45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly
 50          55          60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp
 65          70          75          80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met
          85          90          95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser
 100          105          110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala
 115          120          125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe
 130          135          140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe
 145          150          155          160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser
          165          170          175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln
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<210> 19

<211> 24

<212> DNA

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 19

tgctgtgcta ctcctgcaaa gccc

24

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 20

tgcaacaagtc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 21

agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

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<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

<400> 23

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Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu
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          20          25          30
Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser
          35          40          45
Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
          50          55          60
Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp
          65          70          75          80
Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr
          85          90          95
Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
          100          105          110
Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr
          115          120          125
Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg
          130          135          140
Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu
          145          150          155          160
Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn
          165          170          175
His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr
          180          185          190
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<210> 24

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 24

cagtacgtga gggaccaggg cgccatga

28

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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ccggtgacct gcacgtgctt gcca

24

&lt;210&gt; 26

&lt;211&gt; 41

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;220&gt;

&lt;221&gt; modified\_base

&lt;222&gt; (21)..(21)

&lt;223&gt; a, t, c or g

&lt;400&gt; 26

gcggatctgc cgctgtctca nctggctcgg catggcgccc t

41

&lt;210&gt; 27

&lt;211&gt; 2479

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 27

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<210> 28  
<211> 660  
<212> PRT  
<213> Homo sapiens

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Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr  
35 40 45  
Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly  
50 55 60  
Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe  
65 70 75 80  
Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr  
85 90 95  
Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg  
100 105 110  
Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala  
115 120 125  
Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser  
130 135 140  
Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser  
145 150 155 160  
Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val  
165 170 175  
Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile  
180 185 190  
Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg  
195 200 205  
Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly  
210 215 220  
Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn  
225 230 235 240  
Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg  
245 250 255  
Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe  
260 265 270

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp  
 305 310 315 320  
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly  
 325 330 335  
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu  
 340 345 350  
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 370 375 380  
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro  
 385 390 395 400  
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg  
 405 410 415  
 Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val  
 420 425 430  
 Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met  
 435 440 445  
 Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly  
 450 455 460  
 Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu  
 465 470 475 480  
 Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu  
 485 490 495  
 Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala  
 500 505 510  
 Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser  
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 His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala  
 530 535 540  
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 545 550 555 560  
 Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys  
 565 570 575  
 Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly  
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 Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln  
 595 600 605

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu  
610 615 620

Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His  
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Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu  
645 650 655

His Cys His Thr  
660

<210> 29  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 29  
cggctctacct gtatggcaac c 21

<210> 30  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 30  
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<210> 31  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 31  
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<210> 32  
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<212> DNA  
<213> Artificial Sequence

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oligonucleotide probe

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<210> 33  
<211> 3449  
<212> DNA



&lt;213&gt; Homo sapiens

&lt;400&gt; 33

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tctgtgaagc tctagaagac tccgatggaa gacaggactc tccagcaggg gaactgccaa 2640
aaacggtcca acagccaaca gaatctgagc cagtccacct aaatatccaa gacctacttt 2700
cctgttctaa ttttgagtg caacacagat atctgtttga agaagacaat cttttacggg 2760
ctacacaaaa gctttcccat tcaacaaaac cttcaggaag ccctttggaa gaaaaacacg 2820
atcaatgcaa atgtgaaaaa cttataatgt tccagaacct tgcaaacgaa gaagtaagaa 2880
aattaacaca gcgcttagaa gaaatgacac agagaatgga agccctggaa aatcgctga 2940
gatacagatg aagattagaa atcgcgacac atttgtagtc attgtatcac ggattacaat 3000
gaacgcagtg cagagcccca aagctcaggc tattgttaaa tcaataatgt tgtgaagtaa 3060
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gaatgaataa gctatgcaag gtattttgta atatactgtg gacacaactt gcttctgcct 3240
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&lt;210&gt; 34

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;211&gt; 915

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 34

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Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile
 1          5          10          15
Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile
          20          25          30
Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu
          35          40          45
Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser
          50          55          60
Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile
          65          70          75          80
Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
          85          90          95
Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
          100          105          110
Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg
          115          120          125
His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu
          130          135          140
Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn
          145          150          155          160
Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser
          165          170          175
Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe
          180          185          190
Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
          195          200          205
Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln
          210          215          220
Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His
          225          230          235          240
Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile
          245          250          255
Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser
          260          265          270
Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His
          275          280          285
Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln
          290          295          300
Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala

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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

305                      310                      315                      320  
 Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val  
                                  325                      330                      335  
 Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu  
                                  340                      345                      350  
 Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn  
                                  355                      360                      365  
 Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr  
                                  370                      375                      380  
 Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys  
                                  385                      390                      395                      400  
 Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu  
                                  405                      410                      415  
 Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe  
                                  420                      425                      430  
 Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu  
                                  435                      440                      445  
 Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser  
                                  450                      455                      460  
 Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys  
                                  465                      470                      475                      480  
 Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu  
                                  485                      490                      495  
 His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu  
                                  500                      505                      510  
 Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val  
                                  515                      520                      525  
 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp  
                                  530                      535                      540  
 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp  
                                  545                      550                      555                      560  
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly  
                                  565                      570                      575  
 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys  
                                  580                      585                      590  
 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys  
                                  595                      600                      605  
 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser  
                                  610                      615                      620  
 Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile  
                                  625                      630                      635                      640  
 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
645 650 655

Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn  
660 665 670  
Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly  
675 680 685  
Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser  
690 695 700  
Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg  
705 710 715 720  
Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu  
725 730 735  
Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly  
740 745 750  
Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro  
755 760 765  
Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu  
770 775 780  
Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser  
785 790 795 800  
Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln  
805 810 815  
Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu  
820 825 830  
Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp  
835 840 845  
Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser  
850 855 860  
Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu  
865 870 875 880  
Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln  
885 890 895  
Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu  
900 905 910  
Arg Tyr Arg  
915

<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 35

<210> 36  
 <211> 22  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 36  
 acagccatgg tctatagctt gg 22

<210> 37  
 <211> 45  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 37  
 gcctgtcagt gtcctgaggg acacgtgctc cgcagc gatg ggaag 45

<210> 38  
 <211> 1813  
 <212> DNA  
 <213> Homo sapiens

<400> 38  
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 cggcacctgc aggtccgtgc gtcccgcggc tggcgcccct gactccgtcc cggccaggga 120  
 gggccatgat ttccctcccg gggcccctgg tgaccaactt gctgcggttt ttgttcctgg 180  
 ggctgagtgc cctcgcgccc ccctcgcggg ccagctgca actgcacttg cccgccaacc 240  
 ggttgagggc ggtggagggg ggggaagtgg tgcttcagc gtggtacacc ttgcacgggg 300  
 aggtgtcttc atcccagcca tgggaggtgc cctttgtgat gtggttcttc aaacagaaaag 360  
 aaaaggagga tcaggtgttg tcctacatca atgggggtcac aacaagcaaa cctggagtat 420  
 ccttggtcta ctccatgccc tcccgaacc tgccctcgc gctggagggt ctccaggaga 480  
 aagactctgg cccctacagc tgctccgtga atgtgcaaga caaacaaggc aaatctaggg 540  
 gccacagcat caaaacctta gaactcaatg tactggttcc tccagctcct ccctcctgcc 600  
 gtctccaggg tgtgccccat gtgggggcaa acgtgaccct gagctgccag tctccaaggga 660  
 gtaagcccg tgtccaatac cagtgggatc ggcagcttcc atccttccag actttctttg 720  
 caccagcatt agatgtcatc cgtgggtcct taagcctcac caacctttcg tcttccatgg 780  
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 aaggatttgg ggtctctcct tcctataagg gtcacctcta gcacagaggc ctgagtcattg 1380  
 ggaaagagtc acactcctga cccttagtac tctgccccca cctctcttta ctgtgggaaa 1440  
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 attgggagga gccctccacc acccctgact cctccttatg aagccagctg ctgaaattag 1560  
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 ataacctgtc aggctggctt ggttaggttt tactggggca gaggataggg aatctcttat 1740  
 taaaactaac atgaaatatg tgttgttttc atttgcaaat ttaaataaag atacataatg 1800  
 tttgatgaa aaa 1813

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;210&gt; 39

&lt;211&gt; 390

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 39

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu  
1 5 10 15Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln  
20 25 30Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val  
35 40 45Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln  
50 55 60Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys  
65 70 75 80Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro  
85 90 95Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg  
100 105 110Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val  
115 120 125Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr  
130 135 140Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu  
145 150 155 160Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser  
165 170 175Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro  
180 185 190Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser  
195 200 205Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys  
210 215 220Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu  
225 230 235 240Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly  
245 250 255Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His  
260 265 270Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp  
275 280 285Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile  
290 295 300

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg  
 305 310 315 320  
 Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
 325 330 335  
 Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly  
 340 345 350  
 Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser  
 355 360 365  
 Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
 370 375 380  
 Gln Ala Gly Ser Leu Val  
 385 390

<210> 40  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 40  
 aggtctcca ggagaaagac tc 22

<210> 41  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 41  
 attgtgggcc ttgcagacat agac 24

<210> 42  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 42  
 gccacagca taaaacctt agaactcaat gtactggttc ctccagctcc 50

<210> 43  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 43  
gtgtgacaca gcgtgggc 18

<210> 44  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 44  
gaccggcagg cttctgcg 18

<210> 45  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 45  
cagcagcttc agccaccagg agtgg 25

<210> 46  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 46  
ctgagccgtg ggctgcagtc tcgc 24

<210> 47  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 47  
ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc 45

<210> 48  
<211> 2822  
<212> DNA  
<213> Homo sapiens

<400> 48  
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gtgaaatcgc caatggaatt gaagcctgct attgcaacat gggattttca ggaaatgggtg 180  
tcacaatttg tgaagatgat aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg 240  
ctaattgcac taacacagaa ggaagttatt attgtatgtg tgtacctggc ttcagatcca 300



## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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gcagtaacca agacagggtt atcactaatg atggaaccgt ctgtatagaa aatgtgaatg 360
caaactgccg tttagataat gtctgtatag ctgcaaatat taataaaact ttaacaaaaa 420
tcagatccat aaaagaacct gtggctttgc tacaagaagt ctatagaaat tctgtgacag 480
atctttcacc aacagatata attacatata tagaaatatt agctgaatca tcttcattac 540
taggttacaa gaacaacact atctcagcca aggacaccct ttctaactca actcttactg 600
aatgtgtaaa aaccgtgaat aatgtgttgc aaagggatac atttgtagtt tgggacaagt 660
tatctgtgaa tcataggaga acacatctta caaaactcat gcacactgtt gaacaagcta 720
ctttaaggat atcccagagc ttccaaaaga ccacagagtt tgatacaaat tcaacggata 780
tagctctcaa agttttcttt tttgattcat ataacatgaa acatattcat cctcatatga 840
atatggatgg agactacata aatatatttc caaagagaaa agctgcatat gattcaaatg 900
gcaatgttgc agttgcattt ttatatatta agagtattgg tcctttgctt tcatcatctg 960
acaacttctt attgaaacct caaaattatg ataattctga agaggaggaa agagtcatat 1020
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agactttctg ttgctaatac tgtttctttt tctaataattc taaaaaaa aaaggttt 2760
acctccacaa attgaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2822
aa

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&lt;210&gt; 49

&lt;211&gt; 690

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 49

```

Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys
 1             5             10             15

```

```

Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
          20             25             30

```

```

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
          35             40             45

```

```

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
          50             55             60

```

```

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly

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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

[illegible]

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
405 410 415

Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln  
420 425 430  
Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr  
435 440 445  
Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys  
450 455 460  
Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly  
465 470 475 480  
Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu  
485 490 495  
Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly  
500 505 510  
Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe  
515 520 525  
Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val  
530 535 540  
Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys  
545 550 555 560  
Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly  
565 570 575  
Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile  
580 585 590  
Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser  
595 600 605  
Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu  
610 615 620  
Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His  
625 630 635 640  
Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln  
645 650 655  
Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln  
660 665 670  
Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys  
675 680 685  
Leu Arg  
690

<210> 50  
<211> 589  
<212> DNA  
<213> Homo sapiens  
<220>  
<221> modified\_base

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<222> (61)..(61)

<223> a, t, c or g

<400> 50

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gtattggtcc	ctttgccttc	atcatctgac	aacttcttat	tgaaacctca	aaattatgat	180
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gataggata	ggagtctatg	tggcattttg	gaatactcac	ctgataccat	gaatggcagc	360
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tataatattc	ttacaaggat	cactcaacta	ggaataatta	tttactgat	ttgtcttgcc	540
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<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 51

ggtaatgagc tccattacag

20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 52

ggagtagaaa gcgcatgg

18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag

22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 55  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 55  
ggatctcctg agctcagg 18

<210> 56  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 56  
cctagttgag tgatccttgt aag 23

<210> 57  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 57  
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<210> 58  
<211> 2137  
<212> DNA  
<213> Homo sapiens

<400> 58  
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tgctgccagg ggctgtggtg cctgcagcgt gggggacgtg cttctacaag aacagtcctg 1200  
agtccacgtt ctgtttagct ttaggaagaa acatctagaa gttgtacata ttcagagttt 1260

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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gctgcactgt ctgagttctg ctggaatacc tccatcgatg ggggaactcac ttcctttgga 1440
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cagaagacag gcagtagttt taatttcagg aacagggtgat ccactctgta aaacagcagg 1560
taaatttcac tcaaccccat gtgggaattg atctatatct ctacttccag ggaccatttg 1620
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ggccagttct gtcatggatg ctgtcctgag aataacttgc tgtcccgtg tcacctgctt 1800
ccatctccca gccaccagc cctctgccca cctcacatgc ctccccatgg attggggcct 1860
cccaggcccc ccaccttatg tcaacctgca cttcttgttc aaaaatcagg aaaagaaaag 1920
atttgaagac cccaagtctt gtcaataact tgctgtgtgg aagcagcggg ggaagacctt 1980
gaaccctttc ccagcactt ggttttccaa catgatattt atgagtaatt tattttgata 2040
tgtacatctc ttattttctt acattattta tgcccccaa ttatatttat gtatgtaagt 2100
gaggtttggt ttgtatatta aaatggagtt tgtttgt 2137

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&lt;210&gt; 59

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 59

```

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
 1          5          10          15
Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
          20          25          30
His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
          35          40          45
Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
          50          55          60
Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
          65          70          75          80
Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
          85          90          95
Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
          100          105          110
Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro
          115          120          125
Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
          130          135          140
Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
          145          150          155          160
Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
          165          170          175
Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
          180          185          190
Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
          195          200          205
Val Arg Ser Pro Ser Phe Glu Lys
          210          215

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 60  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 60  
 atccgcccag atggctacaa tgtgta 26

<210> 61  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 61  
 gcctcccggg ctcctgagc agtgccaaac agcggcagtg ta 42

<210> 62  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 62  
 ccagtccggg gacaagccca aa 22

<210> 63  
 <211> 1295  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
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 gctgctgctg cgctacctgg tggcgcacct gggctatcat aaggcctatg gggtttctgc 180  
 cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggctatgt tagcctgcaa 240  
 aaccccaaag aagactgttt cctccagatt agagtggaaag aaactgggtc ggagtgtctc 300  
 ctttgtctac tatcaacaga ctcttcaagg tgattttaaa aatcgagctg agatgataga 360  
 tttcaatatc cggatcaaaa atgtgacaag aagtgatgag gggaaatatc gttgtgaagt 420  
 tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tggaaagtatt 480  
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 acccgggagg cggagggtgc agtgagctga gatcagcca ctgcagtcca gcctgggtaa 1200

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
cagagcaaga ttccatctca aaaaataaaa taaataaata aataaatact gggtttttacc 1260  
tgtagaattc ttacaataaaa tatagcttga tattc 1295

<210> 64  
<211> 312  
<212> PRT  
<213> Homo sapiens

<400> 64  
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Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro  
20 25 30  
Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu  
35 40 45  
Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys  
50 55 60  
Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln  
65 70 75 80  
Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  
85 90 95  
Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
100 105 110  
Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu  
115 120 125  
Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser  
130 135 140  
Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly  
145 150 155 160  
Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu  
165 170 175  
Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met  
180 185 190  
Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp  
195 200 205  
Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg  
210 215 220  
Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile  
225 230 235 240  
Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu  
245 250 255  
Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser  
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Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn  
275 280 285



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala  
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Gly Gly Ser Arg Gly Gln Glu Phe  
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<210> 65  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 65  
atcgttgatga agtttagtgcc cc 22

<210> 66  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 66  
acctgcgata tccaacagaa ttg 23

<210> 67  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 67  
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<210> 68  
<211> 2639  
<212> DNA  
<213> Homo sapiens

<400> 68  
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gcatcatgct gctattcctg caaataactga agaagcatgg gatttaataa ttttacttct 180  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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acttacaaga actctatatt aatcacaact tgctttctac aatttcacct ggagccttta 960
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gtaagtgggt tgatgctctt ccaaacttag agattctgat gattggggaa aatccaatta 1080
tcagaatcaa agacatgaac ttttaagcctc ttatcaatct tcgcagcctg gttatagctg 1140
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<210> 69  
 <211> 708  
 <212> PRT  
 <213> Homo sapiens

<400> 69  
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 Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met  
 35 40 45  
 Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro  
 50 55 60  
 Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn  
 65 70 75 80  
 Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly  
 85 90 95  
 Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val  
 100 105 110  
 Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu  
 115 120 125  
 Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu  
 130 135 140

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe  
 145 150 155 160  
 Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu  
 165 170 175  
 Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile  
 180 185 190  
 Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe  
 195 200 205  
 Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu  
 210 215 220  
 Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser  
 225 230 235 240  
 Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu  
 245 250 255  
 Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile  
 260 265 270  
 Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu  
 275 280 285  
 Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala  
 290 295 300  
 Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro  
 305 310 315 320  
 Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu  
 325 330 335  
 Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly  
 340 345 350  
 Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn  
 355 360 365  
 Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr  
 370 375 380  
 Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro  
 385 390 395 400  
 Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met  
 405 410 415  
 Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu  
 420 425 430  
 Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala  
 435 440 445  
 Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu  
 450 455 460  
 Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr  
 465 470 475 480

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys  
485 490 495

Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys  
500 505 510

Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys  
515 520 525

Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser  
530 535 540

Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr  
545 550 555 560

Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys  
565 570 575

Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys  
580 585 590

Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn  
595 600 605

Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn  
610 615 620

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile  
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp  
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala  
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys  
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro  
690 695 700

Thr Asn Met Ser  
705

<210> 70  
<211> 1305  
<212> DNA  
<213> Homo sapiens

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ttaccacgct tggttgagta gatgaggaat gggctcgtga ttatgctgac attccagcat 180  
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tgttcttatg atactgtgct ttcattctgc cagtatgtgt cccaagggt gtctttgttc 300  
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aattgccaac aaccctggc actgcgactg tactctacag caagttctga ggagcatggc 660  
gtccaatcat gagacagccc acaacgtgat ctgtaaaacg tccgtgttgg atgaacatgc 720

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<210> 71  
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 <212> PRT  
 <213> Homo sapiens

<400> 71  
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 1 5 10 15  
 Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser  
 20 25 30  
 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val  
 35 40 45  
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
 50 55 60  
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
 65 70 75 80  
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
 85 90 95  
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
 100 105 110  
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
 115 120 125  
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
 130 135 140  
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met  
 145 150 155 160  
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val  
 165 170 175  
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala  
 180 185 190  
 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val  
 195 200 205  
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
 210 215 220  
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
 225 230 235 240  
 Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
245 250 255

Thr Val Val

<210> 72  
<211> 2290  
<212> DNA  
<213> Homo sapiens

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gcctgaagct catcccgtca ggcgtcttca ctggcctcag caacctgacc aagcaggaca 480  
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aaaaaaaaaa 2290

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<211> 620  
<212> PRT  
<213> Homo sapiens

<400> 73  
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Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly  
20 25 30

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys  
35 40 45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala  
50 55 60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys  
65 70 75 80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His  
85 90 95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro  
100 105 110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser  
115 120 125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn  
130 135 140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp  
145 150 155 160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp  
165 170 175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser  
180 185 190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr  
195 200 205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His  
210 215 220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg  
225 230 235 240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr  
245 250 255

Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His  
260 265 270

Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr  
275 280 285

Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly  
290 295 300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly  
305 310 315 320

Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr  
325 330 335

Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu  
340 345 350

Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser  
355 360 365

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg  
 370 375 380  
 Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu  
 385 390 395 400  
 Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro  
 405 410 415  
 Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln  
 420 425 430  
 Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala  
 435 440 445  
 Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His  
 450 455 460  
 Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly  
 465 470 475 480  
 Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu  
 485 490 495  
 Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu  
 500 505 510  
 His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr  
 515 520 525  
 Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr  
 530 535 540  
 Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala  
 545 550 555 560  
 Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu  
 565 570 575  
 Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn  
 580 585 590  
 Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser  
 595 600 605  
 Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile  
 610 615 620

&lt;210&gt; 74

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic oligonucleotide probe

&lt;400&gt; 74

tcacctggag cctttattgg cc

22

&lt;210&gt; 75

&lt;211&gt; 23

&lt;212&gt; DNA



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 75

ataccagcta taaccaggct gcg

23

<210> 76

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 76

caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg  
gg

50

52

<210> 77

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 77

ccatgtgtct cctcctacaa ag

22

<210> 78

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 78

gggaatagat gtgatctgat tgg

23

<210> 79

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 79

cacctgtagc aatgcaaatc tcaaggaaat acctagagat cttcctcctg

50

<210> 80

<211> 22

<212> DNA

<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 80

agcaaccgcc tgaagctcat cc

22

<210> 81

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 81

aaggcgcggt gaaagatgta gacg

24

<210> 82

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 82

gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga

50

<210> 83

<211> 1685

<212> DNA

<213> Homo sapiens

<400> 83

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agccaggagg cgggcccggg agcgcgatgg gggccccagc cgctcgtc ctgctcctgc 180
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ctcccgttg ctccccagcc caccacccc cctgtacaga atgtctgctt tgggtgcggt 1500
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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atctgtctcc aggctggaga ggcaggagcc ctgggggtgag aaaagcaaaa aacaaacaaa 1680  
aaaca 1685

<210> 84  
<211> 398  
<212> PRT  
<213> Homo sapiens

<400> 84  
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1 5 10 15  
Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln  
20 25 30  
Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu  
35 40 45  
Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn  
50 55 60  
Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp  
65 70 75 80  
Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser  
85 90 95  
Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile  
100 105 110  
Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly  
115 120 125  
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130 135 140  
Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala  
145 150 155 160  
Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro  
165 170 175  
Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser  
180 185 190  
Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val  
195 200 205  
Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser  
210 215 220  
Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp  
225 230 235 240  
Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly  
245 250 255  
Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser  
260 265 270  
Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe  
275 280 285

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
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 Pro Val Pro Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
 325 330 335  
 Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly  
 340 345 350  
 His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys  
 355 360 365  
 Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
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 Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
 385 390 395

<210> 85  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 85  
 gctaggaatt ccacagaagc cc 22

<210> 86  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 86  
 aacctggaat gtcaccgagc tg 22

<210> 87  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 87  
 cctagcacag tgacgagggg cttggc 26

<210> 88  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 88

aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc

50

&lt;210&gt; 89

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 89

gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt

50

&lt;210&gt; 90

&lt;211&gt; 2755

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 90

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tagaaaagat ttaactgtct tctccaatga cgagatctgc cctcagctgt acgctaggat 1920
ctgccccagc ttaacttcgc acagtaaaaa cagcactggg ttggcggaga ccgggacgca 1980
ctccaactcc tacctagaca ccagcagggt gtccatctcg gtgttgggtc cgggactgct 2040
gctggtgttt gtcacctccg cttcaccgt ggtgggcatg ctctgtttta tcctgaggaa 2100
ccgaaagcgg tccaagagac gagatgccaa ctctcccg tccgagatta attccctaca 2160
gacagtctgt gactcttcct actggcacia tgggccttac aacgcagatg gggcccacag 2220
agtgtatgac tgtggctctc actcgctctc agactaagac cccaaccca ataggggagg 2280

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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gcagaggggaa ggcgatacat ctttccccac cgcaggcacc ccgggggctg gaggggctg 2340
taccCAAATC CCCGCGCCAT CAGCCTGGAT GGGCATAAGT AGATAAATAA CTGTGAGCTC 2400
gcacaaccga aagggcctga ccccttactt agctccctcc ttgaaacaaa gagcagactg 2460
tgagagctg ggagagcgca gccagctcgc tctttgctga gagccccctt tgacagaaag 2520
cccagcacga ccctgctgga agaactgaca gtgccctcgc cctcggcccc ggggcctgtg 2580
gggttgatg ccgcggttct atacatatat acatatatcc acatctatat agagagatag 2640
atatctattt ttcccctgtg gattagcccc gtgatggctc cctgttggct acgcagggat 2700
gggcagttgc acgaaggcat gaatgtattg taaataagta actttgactt ctgac 2755
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<210> 91  
 <211> 696  
 <212> PRT  
 <213> Homo sapiens

<400> 91  
 Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala  
 1 5 10 15  
 Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn  
 20 25 30  
 Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr  
 35 40 45  
 Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe  
 50 55 60  
 Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn  
 65 70 75 80  
 Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu  
 85 90 95  
 Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His  
 100 105 110  
 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly  
 115 120 125  
 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp  
 130 135 140  
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile  
 145 150 155 160  
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr  
 165 170 175  
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu  
 180 185 190  
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu  
 195 200 205  
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys  
 210 215 220  
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val  
 225 230 235 240  
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr  
 245 250 255

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro  
 260 265 270  
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr  
 275 280 285  
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala  
 290 295 300  
 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg  
 305 310 315 320  
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala  
 325 330 335  
 Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly  
 340 345 350  
 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala  
 355 360 365  
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp  
 370 375 380  
 Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
 385 390 395 400  
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn  
 405 410 415  
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser  
 420 425 430  
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn  
 435 440 445  
 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro  
 450 455 460  
 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
 465 470 475 480  
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu  
 485 490 495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
 500 505 510  
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
 515 520 525  
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala  
 530 535 540  
 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr  
 545 550 555 560  
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
 565 570 575  
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His  
 580 585 590

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
595 600 605

Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
610 615 620

Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
625 630 635 640

Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
645 650 655

Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr  
660 665 670

Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp  
675 680 685

Cys Gly Ser His Ser Leu Ser Asp  
690 695

<210> 92  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 92  
gttgatctg ggcaacaata ac 22

<210> 93  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 93  
attgttgtgc aggctgagtt taag 24

<210> 94  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 94  
ggtggctata catggatagc aattacctgg acacgctgtc ccggg 45

<210> 95  
<211> 2226  
<212> DNA  
<213> Homo sapiens

<400> 95



## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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agtcgactgc gtccctgtta cccggcgcca gctgtgttcc tgaccccaga ataactcagg 60
gctgcaccgg gcctggcagc gctccgcaca catttcctgt cgcgccctaa gggaaactgt 120
tggccgctgg gcccgcgggg ggattcttgg cagttggggg gtccgctcgg agcgaggggc 180
gaggggaagg gagggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240
ccagacacag ctctgcgtcc tcgagcggga cagatccaag ttgggagcag ctctgcgtgc 300
ggggcctcag agaattgaggc cggcgcttcg cctgtgcctc ctctggcagg cgctctggcc 360
cgggccgggc ggcggcgaac accccactgc cgaccgtgct ggctgctcgg cctcgggggc 420
ctgctacagc ctgcaccacg ctaccatgaa gcggcaggcg gccgaggagg cctgcatcct 480
gcgaggtggg gcgctcagca ccgtgcgtgc gggcgccgag ctgcgcgctg tgctcgcgct 540
cctgcgggga ggcccagggc ccggaggggg ctccaaaagac ctgctgttct gggtcgcact 600
ggagcgcagg cgttccctact gcaccctgga gaacgagcct ttgcgggggt tctcctggct 660
gtcctccgac cccggcggtc tcgaaagcga cacgctgcag tgggtggagg agccccaacg 720
ctcctgcacc gcgcggagat gcgcggtact ccaggccacc ggtggggctg agcccgagg 780
ctggaaggag atgcgatgcc acctgcgcgc caacggctac ctgtgcaagt accagtttga 840
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ccagctgcac agcgcgcctc tggacttcag tccactggg accgaggtga gtgcgctctg 960
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cgcagagctc cctaactgcc tagacgactt gggaggcttt gcctgcgaat gtgctacggg 1140
cttcgagctg ggggaaggag gccgctcttg tgtgaccagt ggggaaggac agccgacctt 1200
tggggggacc ggggtgccc caggcgccc gccggccact gcaaccagcc ccgtgccgca 1260
gagaacatgg ccaatcaggg tcgacgagaa gctgggagag acaccacttg tccctgaaca 1320
agacaattca gtaacatcta ttcctgagat tcctcgatgg ggatcacaga gcacgatgtc 1380
tacccttcaa atgtcccttc aagccgagtc aaaggccact atcaccatcag cagggagcgt 1440
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ttgtgtaact gacaatttct gcagaaatcc cccttcctct aaattccctt tactccactg 1920
aggagctaaa tcagaactgc acactccttc cctgatgata gaggaagtgg aagtgccttt 1980
aggatggtag tactggggga ccgggtagtg ctggggagag atattttctt atgtttattc 2040
ggagaatttg gagaagtgat tgaacttttc aagacattgg aaacaaatag aacacaatat 2100
aatttacatt aaaaaataat ttctaccaa atggaaagga aatgttctat gttgttcagg 2160
ctaggagtat attggttcga aatcccaggg aaaaaataa aaataaaaaa ttaaaggatt 2220
gttgat 2226

```

&lt;210&gt; 96

&lt;211&gt; 490

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 96

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Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
 1           5           10           15
Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser
          20           25           30
Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
          35           40           45
Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
          50           55           60
Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly
          65           70           75           80
Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu
          85           90           95

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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly  
 100 105 110  
 Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu  
 115 120 125  
 Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala  
 130 135 140  
 Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met  
 145 150 155 160  
 Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu  
 165 170 175  
 Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr  
 180 185 190  
 Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro  
 195 200 205  
 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val  
 210 215 220  
 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly  
 225 230 235 240  
 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys  
 245 250 255  
 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu  
 260 265 270  
 Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr  
 275 280 285  
 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg  
 290 295 300  
 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro  
 305 310 315 320  
 Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln  
 325 330 335  
 Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln  
 340 345 350  
 Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala  
 355 360 365  
 Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr  
 370 375 380  
 Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe  
 385 390 395 400  
 Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr  
 405 410 415  
 Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln  
 420 425 430

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu  
 435 440 445

Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val  
 450 455 460

Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu  
 465 470 475 480

Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala  
 485 490

<210> 97  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 97  
 tggaaggaga tgcgatgccca cctg 24

<210> 98  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 98  
 tgaccagtgg ggaaggacag 20

<210> 99  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 99  
 acagagcaga ggggtgccttg 20

<210> 100  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 100  
 tcagggacaa gtggtgtctc tccc 24

<210> 101  
 <211> 24  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 101

tcaggggaagg agtgtgcagt tctg

24

<210> 102

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 102

acagctcccg atctcagtta cttgcatcgc ggacgaaatc ggcgctcgct

50

<210> 103

<211> 2026

<212> DNA

<213> Homo sapiens

<400> 103

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agcgtcgagt	cagacggcac	cataatcgcc	tttaaaagtg	cctccgccct	gccggccgcg	120
tatcccccg	ctacctgggc	cgccccgcgg	cggtgcgcgc	gtgagaggga	gcgcgcgggc	180
agccgagcgc	cggtgtgagc	cagcgcgtgt	gccagtgtga	gcggcgggtg	gagcgcgggtg	240
ggtgcggagg	ggcgtgtgtg	ccggcgcgcg	cgccgtgggg	tgcaaacc	gagcgtctac	300
gctgccatga	ggggcgcgaa	cgccgtgggc	ccactctgcc	tgctgtggc	tgccgccacc	360
cagctctcgc	ggcagcagtc	cccagagaga	cctgttttca	catgtggtgg	cattcttact	420
ggagagtctg	gatttattgg	cagtgaaggt	tttcctggag	tgtaccctcc	aaatagcaaa	480
tgtacttgga	aaatcacagt	tcccgaagga	aaagtagtcg	ttctcaattt	ccgattcata	540
gacctcgaga	gtgacaacct	gtgccgctat	gactttgtgg	atgtgtacaa	tggccatgcc	600
aatggccagc	gcattggccg	cttctgtggc	actttccggc	ctggagccct	tgtgtccagt	660
ggcaacaaga	tgatggtgca	gatgatttct	gatgccaa	cagctggcaa	tggcttcagt	720
gccatgttct	ccgctgctga	accaaacgaa	agaggggatc	agtattgtgg	aggactcctt	780
gacagacctt	ccggctcttt	taaaaccccc	aactggccag	accgggatta	ccctgcagga	840
gtcacttggtg	tgtggcacat	tgtagcccca	aagaatcagc	ttatagaatt	aaagtttgag	900
aagtttgatg	tggagcgaga	taactactgc	cgatatgatt	atgtggctgt	gtttaatggc	960
ggggaagtca	acgatgctag	aagaattgga	aagtattgtg	gtgatagtcc	acctgcgcca	1020
attgtgtctg	agagaaatga	acttcttatt	cagtttttat	cagacttaag	tttaactgca	1080
gatgggttta	ttggctacta	catattcagg	ccaaaaaaac	tgcttacaac	tacagaacag	1140
cctgtcacca	ccacattccc	tgtaccacag	ggtttaaaac	ccaccgtggc	cttgtgtcaa	1200
caaaagtgtg	gacggacggg	gactctggag	ggcaattatt	gttcaagtga	ctttgtatta	1260
gccggcactg	ttatcacaa	catcactcgc	gatgggagtt	tgacgcccac	agtctcgatc	1320
atcaacatct	acaaagaggg	aaatttgccg	attcagcagg	cgggcaagaa	catgagtgcc	1380
aggctgactg	tcgtctgcaa	gcagtgccct	ctcctcagaa	gaggtctaaa	ttacattatt	1440
atggggcaag	taggtgaaga	tgggcgagcc	aaaatcatgc	caaacagctt	tatcatgatg	1500
ttcaagacca	agaatcagaa	gctcctggat	gccttaaaaa	ataagcaatg	ttaacagtga	1560
actgtgtcca	tttaagctgt	attctgccat	tgcccttgaa	agatctatgt	tctctcagta	1620
gaaaaaaaaa	tacttataaa	attacatatt	ctgaaagagg	attccgaaag	atgggactgg	1680
ttgactcttc	acatgatgga	ggtatgaggc	ctccgagata	gctgagggaa	gttctttgcc	1740
tgctgtcaga	ggagcagcta	tctgattgga	aacctgccga	cttagtgcgg	tgataggaag	1800
ctaaaagtgt	caagcgttga	cagcttgga	gcgtttat	atacatctct	gtaaaaagga	1860
attttagaat	tgagttgtgt	gaagatgtca	aaaaaagatt	ttagaagtgc	aatattttata	1920
gtgttatgtg	tttcaccttc	aagcctttgc	cctgaggtgt	tacaatcttg	tcttgcgttt	1980
tctaaatcaa	tgcttaataa	aatattttta	aaggaaaaaa	aaaaaa		2026

<210> 104

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

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Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
 1           5           10           15
Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
          20           25           30
Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
      35           40           45
Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
      50           55           60
Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu
      65           70           75           80
Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
          85           90           95
His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro
      100           105           110
Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser
      115           120           125
Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala
      130           135           140
Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg
      145           150           155           160
Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro
          165           170           175
Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu
      180           185           190
Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys
      195           200           205
Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala
      210           215           220
Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val
      225           230           235           240
Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu
          245           250           255
Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu
      260           265           270
Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr
      275           280           285
Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr
      290           295           300
Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly

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305                    310                    315                    320  
 Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val  
                          325                    330                    335  
 Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala  
                          340                    345                    350  
 Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro  
                          355                    360                    365  
 Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu  
                          370                    375                    380  
 Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys  
 385                    390                    395                    400  
 Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys  
                          405                    410                    415

<210> 105  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
                          oligonucleotide probe

<400> 105  
 ccgattcata gacctcgaga gt 22

<210> 106  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
                          oligonucleotide probe

<400> 106  
 gtcaaggagt cctccacaat ac 22

<210> 107  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
                          oligonucleotide probe

<400> 107  
 gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt 45

<210> 108  
 <211> 1838  
 <212> DNA  
 <213> Homo sapiens

<400> 108  
 cggacgcgtg ggcggacgcg tgggcggccc acggcgcccc cgggctgggg cggtcgcttc 60

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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ttcctttctcc gtggcctacg aggggtcccca gcctgggtaa agatggcccc atggcccccg 120
aagggcctag tcccagctgt gctctggggc ctcagcctct tcctcaacct cccaggacct 180
atctggctcc agccctctcc acctcccccag tcttctcccc cgctcagcc ccatccgtgt 240
catacctgcc ggggactggt tgacagcttt aacaagggcc tggagagaac catccgggac 300
aactttggag gtggaacacac tgcctgggag gaagagaatt tgtccaaata caaagacagt 360
gagacccgcc tggtagaggt gctggagggt gtgtgcagca agtcagactt cgagtgccac 420
cgctgctgg agctgagtga ggagctgggt gagagctggt ggtttcacaa gcagcaggag 480
gccccggacc tcttccagtg gctgtgctca gattccctga agctctgctg ccccgagggc 540
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ggtcttgtaa agttaaaaaa aaaaaaaaaa aaaaaaaaa 1838

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&lt;210&gt; 109

&lt;211&gt; 420

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 109

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Met Ala Pro Trp Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
  1           5           10          15
Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
      20           25           30
Pro Pro Pro Gln Ser Ser Pro Pro Gln Pro His Pro Cys His Thr
      35           40           45
Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
      50           55           60
Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu
      65           70           75           80
Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly
      85           90           95
Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser
      100          105          110
Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro
      115          120          125
Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro
      130          135          140

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu  
145 150 155 160  
Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly  
165 170 175  
Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys  
180 185 190  
Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His  
195 200 205  
Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro  
210 215 220  
Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His  
225 230 235 240  
Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys  
245 250 255  
Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg  
260 265 270  
Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg  
275 280 285  
Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu  
290 295 300  
Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln  
305 310 315 320  
Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr  
325 330 335  
Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala  
340 345 350  
Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
355 360 365  
Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
370 375 380  
Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
385 390 395 400  
Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
405 410 415  
Ile Lys Gly Arg  
420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 110  
cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga 50

<210> 111  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 111  
attctgcgtg aacactgagg gc 22

<210> 112  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 112  
atctgcttgt agccctcggc ac 22

<210> 113  
<211> 1616  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1461)..(1461)  
<223> a, t, c or g

<400> 113  
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cagcaccatg cagccccctgt ggctctgctg ggcactctgg gtgttgcccc tggccagccc 120  
cggggccgccc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180  
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gctggtgttc ggcatggagc agcggctgcc gcccaacagc gagctggtgc aggccgtgct 420  
gcggctcttc caggagccgg tccccaaggc cgcgctgcac aggcacgggc ggctgtcccc 480  
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cgacgtgacc gaggccgtga acttctggca gcagctgagc cggccccggc agccgctgct 660  
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ccaggtggtc agcctgcccc acatgagggt gcagaagtgc agctgtgcct cggatgggtc 1140  
gtcgtgtcca aggaggctcc agccataggc gcctagtgtg gccatcgagg gacttgactt 1200  
gtgtgtgttt ctgaagtgtt cgagggtacc aggagagctg gcgatgactg aactgctgat 1260  
ggacaaatgc tctgtgctct ctagttagcc ctgaatttgc ttcctctgac aagttacctc 1320  
acctaatttt tgcttctcag gaatgagaat ctttggccac tggagagccc ttgctcagtt 1380  
ttctctattc ttattattca ctgcactata ttctaagcac ttacatgtgg agatactgta 1440

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

acctgagggc agaaagccca ntgtgtcatt gtttacttgt cctgtcactg gatctgggct 1500  
aaagtcctcc accaccactc tggacctaag acctgggggtt aagtgtgggt tgtgcatccc 1560  
caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616

<210> 114  
<211> 366  
<212> PRT  
<213> Homo sapiens

<400> 114  
Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala  
1 5 10 15  
Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu  
20 25 30  
Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
35 40 45  
Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu  
50 55 60  
Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln  
65 70 75 80  
Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr  
85 90 95  
His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu  
100 105 110  
Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala  
115 120 125  
Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg  
130 135 140  
Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr  
145 150 155 160  
Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys  
165 170 175  
Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg  
180 185 190  
Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu  
195 200 205  
Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln  
210 215 220  
Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu  
225 230 235 240  
Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro  
245 250 255  
Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu  
260 265 270  
Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe  
275 280 285

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu  
 290 295 300  
 Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu  
 305 310 315 320  
 Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr  
 325 330 335  
 Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser  
 340 345 350  
 Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro  
 355 360 365

<210> 115  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 115  
 aggactgcc a taacttgct g 21

<210> 116  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 116  
 ataggagttg aagcagcgct gc 22

<210> 117  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 117  
 tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc 45

<210> 118  
 <211> 1857  
 <212> DNA  
 <213> Homo sapiens

<400> 118  
 gtctgttccc aggagtcctt cggcggctgt tgtgtcagtg gcctgatcgc gatggggaca 60  
 aaggcgcaag tcgagaggaa actgttgtgc ctcttcatat tggcgatcct gttgtgctcc 120  
 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcctgagaat 180  
 aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtgggaag 240

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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tttgaccaag gagacaccac cagactcgtt tgctataata acaagatcac agcttcctat 300
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actgggacat acacttgatg ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420
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agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa aaaaaaa 1857

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&lt;210&gt; 119

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 119

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile  
1 5 10 15

Leu Ala Ile Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
20 25 30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu  
35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
100 105 110

Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
115 120 125

Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
130 135 140

Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
145 150 155 160

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
165 170 175  
Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
180 185 190  
Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
195 200 205  
Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
210 215 220  
Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
225 230 235 240  
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly  
245 250 255  
Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
260 265 270  
Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
275 280 285  
Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 120

tcgcggagct gtgttctgtt tccc

24

<210> 121

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 121

tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac tggtgtgcct

50

<210> 122

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 122

acacctggtt caaagatggg

20

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 123  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 123  
 taggaagagt tgctgaaggc acgg 24

<210> 124  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 124  
 ttgccttact caggtgctac 20

<210> 125  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 125  
 actcagcagt ggtaggaaag 20

<210> 126  
 <211> 1210  
 <212> DNA  
 <213> Homo sapiens

<400> 126  
 cagcgcgtgg ccggcgccgc tgtggggaca gcatgagcgg cggttggatg ggcgaggttg 60  
 gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctccgactag 120  
 gcctggaggc cgccgcgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180  
 gctcaggctc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240  
 tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgc 300  
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 tgtcctggct ccgagcccag gagcgcctcc gcccactggg gttactggtg gccatgaagg 840  
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 ccgtcactca gccctgggag tagccggaca ggaggagagc agtgatgcgg atgggtaccc 960  
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 agctaggatg gggaaacctgc cacagccaga actgaggggc tggccccagg cagctcccag 1140  
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aagttgcttc

<210> 127  
<211> 282  
<212> PRT  
<213> Homo sapiens

<400> 127  
Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
1 5 10 15  
Leu Gly Leu Ala Leu Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
20 25 30  
Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
35 40 45  
Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
50 55 60  
Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
65 70 75 80  
Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln  
85 90 95  
Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly  
100 105 110  
Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser  
115 120 125  
Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp  
130 135 140  
Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp  
145 150 155 160  
Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly  
165 170 175  
Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser  
180 185 190  
Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val  
195 200 205  
Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly  
210 215 220  
Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala  
225 230 235 240  
Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln  
245 250 255  
Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu  
260 265 270  
Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro  
275 280

<210> 128

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 128  
 aagttccagt gccgcaccag tggc 24

<210> 129  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 129  
 ttggttccac agccgagctc gtcg 24

<210> 130  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 130  
 gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc 50

<210> 131  
 <211> 1843  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1837)..(1837)  
 <223> a, t, c or g

<400> 131  
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 cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccgga 180  
 gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240  
 gactcttggc cgtgatcctg tggtttcagc tggcgctgtg cttcggccct gcacagctca 300  
 cgggcggggt cgatgacctt caagtgtgtg ctgaccccg cttcccgag aatggcttca 360  
 ggacccccag cggagggggt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420  
 gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480  
 gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatac 540  
 aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgtc 600  
 atgaaggatt caagatccgg taccccgacc tacacaatat ggtttcatta tgtcgcgatg 660  
 atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720  
 atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780  
 atcgtgtgct tcccggattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840  
 ttatctggtc gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900  
 ctccaatggt gagtacgga gatttcgtct gccacccgcg gccttgtgag cgctacaacc 960  
 acggaactgt ggtggagttt tactgcatc ctggctacag cctcaccagc gactacaagt 1020



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

```

acatcacctg ccagtatgga gagggtgttc cttcttatca agtctactgc atcaaatacag 1080
agcaaacgtg gcccagcacc catgagaccc tcctgaccac gtggaagatt gtggcggttca 1140
cggcaaccag tgtgctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200
agttcaaggc ccactttccc cccagggggc ctccccggag ttccagcagt gaccctgact 1260
ttgtggtggt agacggcggtg cccgtcatgc tcccgtccta tgacgaagct gtgagtggcg 1320
gcttgagtgc cttaggcccc gggtagatgg cctctgtggg ccagggtgc cccttaccg 1380
tggacgacca gagcccccca gcataccccg gctcagggga cacggacaca ggcccagggg 1440
agtcagaaac ctgtgacagc gtctcaggct cttctgagct gtcctaaagt ctgtattcac 1500
ctcccagggtg ccaagagagc acccaccctg cttcggacaa ccctgacata attgccagca 1560
cggcagagga ggtggcatcc accagcccag gcattccatca tgcccactgg gtgttgttcc 1620
taagaaactg attgattaaa aaatttccca aagtgtctct tcaaatacat 1680
gttgatctgt ggagttgatt cttttccttc tcttggtttt agacaaatgt aaacaaagct 1740
ctgatcctta aaattgctat gctgatagag tggtagaggc tggaagcttg atcaagtcct 1800
gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

```

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

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Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln
 1          5          10          15
Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val
          20          25          30
Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr
          35          40          45
Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
          50          55          60
Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val
          65          70          75          80
Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
          85          90          95
Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser
          100          105          110
Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu
          115          120          125
Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile
          130          135          140
Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn
          145          150          155          160
Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile
          165          170          175
Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn
          180          185          190
Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr
          195          200          205
Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys
          210          215          220

```

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu  
 225 230 235 240  
 Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe  
 245 250 255  
 Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val  
 260 265 270  
 Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr  
 275 280 285  
 Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys  
 290 295 300  
 Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr  
 305 310 315 320  
 Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu  
 325 330 335  
 Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His  
 340 345 350  
 Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe  
 355 360 365  
 Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala  
 370 375 380  
 Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val  
 385 390 395 400  
 Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr  
 405 410 415  
 Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys  
 420 425 430  
 Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro  
 435 440 445  
 Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile  
 450 455 460  
 Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
 465 470 475 480  
 His Ala His Trp Val Leu Phe Leu Arg Asn  
 485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 133

atctcctatc gctgctttcc cgg

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 134  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 134  
 agccaggatc gcagtaaaac tcc

23

<210> 135  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 135  
 atttaaactt gatgggtctg cgtatcttga gtgcttaca aaccttatct

50

<210> 136  
 <211> 1815  
 <212> DNA  
 <213> Homo sapiens

<400> 136  
 cccacgcgtc cgctccgcgc cctccccccc gcctcccgctg cggctccgtcg gtggcctaga 60  
 gatgctgctg ccgcgggttg agttgtcgcg cagcctctg cccgccagcc cgctccaccg 120  
 ccgtagcgcc cgagtgtcgg ggggcgcacc cgagtgcggc catgaggccg ggaaccgcgc 180  
 tacaggccgt gctgctggcc gtgctgctgg tgggctgctg ggccgcgacg ggtcgctgc 240  
 tgagtgcctc ggatttggac ctgagaggag ggcagccagt ctgccgggga gggacacaga 300  
 ggcttctgta taaagtcatt tacttccatg atacttctcg aagactgaac tttaggaag 360  
 ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420  
 agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatgggtgac ttctggattg 480  
 ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540  
 ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcggca 600  
 gcgaggctcg cgtggctatg taccatcagc catcggcacc cgctggcatc ggaggcccct 660  
 acatgttcca gtggaatgat gaccgggtgca acatgaagaa caatttcatt tgcaaatatt 720  
 ctgatgagaa accagcagtt ctttctagag aagctgaagg tgaggaaaca gagctgacaa 780  
 cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840  
 gagaagctgc cttgaatctg gcctacatcc taatccccag cattccccct ctctctctcc 900  
 ttgtggctac cacagttgta tgttgggttt ggatctgtag aaaaagaaaa cgggagcagc 960  
 cagaccctag cacaaagaag caacacacca tctggccctc tcctcaccag ggaaacagcc 1020  
 cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagacc 1080  
 ggccagacct gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140  
 tgtcttctga ctatgacaac atggctgtga acccatcaga aagtgggttt gtgactctgg 1200  
 tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccca gaccaaattg 1260  
 ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacatataaa 1320  
 aaactgaaac tgacaacaat ggaaaagaaa tgataagcaa aatcctctta ttttctataa 1380  
 ggaaaatata cagaaggtct atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440  
 tccccacgac ctctgttgg accccacgt tttggctgta tcctttatcc cagccagtca 1500  
 tccagctcga ctttatgaga aggtaccttg cccaggctcg gcacatagta gactctcaat 1560  
 aaatgtcact tgggttgggt tatctaactt ttaagggaca gagctttacc tggcagtgat 1620  
 aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680  
 atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740  
 ttggcctgtg catcggaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800  
 agcaggaaaa aaaaa 1815

<210> 137

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;211&gt; 382

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu  
 1 5 10 15  
 Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu  
 20 25 30  
 Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro  
 35 40 45  
 Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe  
 50 55 60  
 Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser  
 65 70 75 80  
 Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn  
 85 90 95  
 Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu  
 100 105 110  
 Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr  
 115 120 125  
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser  
 130 135 140  
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro  
 145 150 155 160  
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys  
 165 170 175  
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala  
 180 185 190  
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro  
 195 200 205  
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys  
 210 215 220  
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser  
 225 230 235 240  
 Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val  
 245 250 255  
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys  
 260 265 270  
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp  
 275 280 285  
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala  
 290 295 300  
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

305                      310                      315                      320  
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
                                  325                      330                      335  
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
                                  340                      345                      350  
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
                                  355                      360                      365  
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
                                  370                      375                      380

<210> 138  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 138  
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50.

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 139  
 aagccaaaga agcctgcagg aggg 24

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 140  
 cagtccaagc ataaagggtcc tggc 24

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60  
 gcatccgcag gttcccgcgg acttgggggc gcccgctgag ccccggcgcc cgcagaagac 120  
 ttgtgtttgc ctctgcagc ctcaacccgg agggcagcga gggcctacca ccatgatcac 180  
 tgggtgtgtc agcatgcgct tgtggacccc agtgggcgtc ctgacctcgc tggcgtactg 240  
 cctgcaccag cggcggtgg ccctggccga gctgcaggag gccgatggcc agtgtccggt 300  
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggctcgtg tttcgacacg gggctcggag 360  
 tcctctcaag ccgctcccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

```

ccccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaaccata 480
ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540
gctgaccaag gtgggcatgc agcaaagtgt tgccttggga gagagactga ggaagaacta 600
tgtggaagac attccccttc ttccaccaac ctccaacca caggaggtct ttattcgttc 660
cactaacatt tttcggaatc tggagtccac ccgttgtttg ctggctgggc ttttccagt 720
tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgatatcc 780
caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840
tttacagcca ggaatctcag aggatttgaa aaagggtgaag gacaggatgg gcattgacag 900
tagtgataaa gtggacttct tcatcctcct ggacaacgtg gctgccgagc aggcacacaa 960
cctcccaagc tgccccatgc tgaagagatt tgcacggatg atcgaacaga gagctgtgga 1020
cacatccttg tacatactgc ccaagggaaga cagggaagt cttcagatgg cagtagggcc 1080
attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgccccga 1140
caagatcaga aagctgtatc tctatgctgc tcatgatgtg accttcatac cgctcttaat 1200
gaccctgggg atttttgacc acaaattggc accgtttgct gttgacctga ccatggaact 1260
ttaccagcac ctggaatcta aggagtgggt tgtgcagctc tattaccacg ggaaggagca 1320
ggtgccgaga ggtgccctg atgggctctg cccgctggac atgttcttga atgccatgtc 1380
agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaaactc aggtgatgga 1440
agttggaaat gaagagtaac tgatttataa aagcaggatg tgttgatttt aaaataaagt 1500
gcctttatac aatg 1514

```

&lt;210&gt; 142

&lt;211&gt; 428

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 142

```

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
  1           5           10           15

```

```

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
          20           25           30

```

```

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
          35           40           45

```

```

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
          50           55           60

```

```

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
          65           70           75           80

```

```

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
          85           90           95

```

```

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
          100           105           110

```

```

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
          115           120           125

```

```

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
          130           135           140

```

```

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
          145           150           155           160

```

```

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
          165           170           175

```

```

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His
          180           185           190

```

```

Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys

```

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

195 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
 210 215 220  
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
 225 230 235 240  
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
 245 250 255  
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
 260 265 270  
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
 275 280 285  
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
 290 295 300  
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
 305 310 315 320  
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
 325 330 335  
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
 340 345 350  
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
 355 360 365  
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
 370 375 380  
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
 385 390 395 400  
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
 405 410 415  
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
 420 425

<210> 143

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
oligonucleotide probe

<400> 144  
gcagctctat taccacggga agga 24

<210> 145  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 145  
tccttcccgt ggtaatagag ctgc 24

<210> 146  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 146  
ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg 45

<210> 147  
<211> 1686  
<212> DNA  
<213> Homo sapiens

<400> 147  
ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60  
cttaaatttc agctcatcac cttcacctgc cttgggtcatg gctctgctat tctccttgat 120  
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctgggtggg 180  
gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240  
gtgtgatgac ggctgggaca ttaaggacgt ggctgtgttg tgccgggagc tgggctgtgg 300  
agctgccagc ggaaccctta gtggtatttt gtatgagcca ccagcagaaa aagagcaaaa 360  
ggtcctcatc caatcagtca gttgcacagg aacagaagat acattggctc agtgtgagca 420  
agaagaagtt tatgattggt cacatgatga agatgctggg gcatcgtgtg agaaccaga 480  
gagctctttc tccccagtc cagagggtgt caggctggct gacggccctg ggcattgcaa 540  
gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600  
cctccgggcc gcaaagggtg tgtgccggca gctgggatgt gggagggtg tactgactca 660  
aaaacgctgc aacaagcatg cctatggccg aaaaccatc tggctgagcc agatgtcatg 720  
ctcaggacga gaagcaaccc ttcaggattg ccttcttggg ccttggggga agaacacctg 780  
caaccatgat gaagacacgt gggtcgaatg tgaagatccc tttgacttga gactagttag 840  
aggagacaac ctctgctctg ggcgactgga ggtgctgcac aagggcgtat ggggctctgt 900  
ctgtgatgac aactggggag aaaaggagga ccagggtgta tgcaagcaac tgggctgtgg 960  
gaagtccctc tctccctcct tcagagaccg gaaatgctat ggccctgggg ttggccgcat 1020  
ctggctggat aatgttcgtt gctcagggga ggagcagtc ctggagcagt gccagcacag 1080  
attttggggg tttcacgact gcacccacca ggaagatgtg gctgtcatct gctcagtgtg 1140  
ggtgggcatc atctaactctg ttgagtgcct gaatagaaga aaaacacaga agaaggagc 1200  
atttactgtc tacatgactg catgggatga acactgatct tcttctgccc ttggactggg 1260  
acttatactt ggtgccccctg attctcaggc cttcagagt ggatcagaac ttacaacatc 1320  
aggctagtgt ctcaggccat cagacatagt ttggaactac atcaccacct ttcctatgtc 1380  
tccacattgc acacagcaga ttcccagcct ccataattgt gtgtatcaac tacttaaata 1440  
cattctcaca cacacacaca cacacacaca cacacatata ccatttgtcc 1500  
tgtttctctg aagaactctg acaaaaataca gattttggta ctgaaagaga ttctagagga 1560  
acggaatttt aaggataaat tttctgaatt ggttatgggg tttctgaaat tggctctata 1620  
atctaattag atataaaatt ctggttaactt tatttacaat aataaagata gcactatgtg 1680



ttcaaa

<210> 148  
<211> 347  
<212> PRT  
<213> Homo sapiens

<400> 148

```

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly
 1           5           10           15
Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
          20           25           30
Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
          35           40           45
Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
          50           55           60
Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
          65           70           75           80
Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
          85           90           95
Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr
          100          105          110
Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
          115          120          125
Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
          130          135          140
Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
          145          150          155          160
Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys
          165          170          175
Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
          180          185          190
Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
          195          200          205
Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
          210          215          220
Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
          225          230          235          240
Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
          245          250          255
Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
          260          265          270
Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
          275          280          285
Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly

```

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

290

295

300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln  
305 310 315 320

Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr  
325 330 335

His Gln Glu Asp Val Ala Val Ile Cys Ser Val  
340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 149

ttcagctcat caccttcacc tgcc

24

<210> 150

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 150

ggctcataca aaataccact aggg

24

<210> 151

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 151

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt

50

<210> 152

<211> 1427

<212> DNA

<213> Homo sapiens

<400> 152

actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctcgacctcg 60  
acccacgcgt ccgcggacgc gtgggcggaac gcgtgggccc gctaccagga agagtctgcc 120  
gaagggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tgttcggctg 180  
cctgggcgtc ttcggcctct tccggctgct gcagtgggtg cgcggaagg cctacctgcg 240  
gaatgctgtg gtggtgatca caggcgccac ctgagggtg ggcaaagaat gtgcaaaagt 300  
cttctatgct gcgggtgcta aactgggtgct ctgtggcccg aatgggtggg ccctagaaga 360  
gctcatcaga gaacttaccg cttctcatgc caccaagggt cagacacaca agccttactt 420  
ggtgaccttc gacctcacag actctggggc catagtgtgca gcagcagctg agatcctgca 480  
gtgctttggc tatgtcgaca tacttgtcaa caatgctggg atcagctacc gtggtaccat 540  
catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccagt 600

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2c1.txt

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tgctctaacg aaagcactcc tgccctccat gatcaagagg aggcaaggcc acattgtcgc 660
catcagcagc atccagggca agatgagcat tccttttcga tcagcatatg cagcctccaa 720
gcacgcaacc caggctttct ttgactgtct gcgtgcccag atggaacagt atgaaattga 780
ggtgaccgtc atcagccccg gctacatcca caccaacctc tctgtaaatg ccatcaccgc 840
ggatggatct aggtatggag ttatggacac caccacagcc cagggccgaa gccctgtgga 900
ggtggccag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960
cttactgcct tccttggtcg tttatcttcg aactctggct cctgggctct tcttcagcct 1020
catggcctcc agggccagaa aagagcggaa atccaagaac tcctagtact ctgaccagcc 1080
agggccaggg cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcat 1140
ttgttgagac tttaatggag atttgtctca caagtgggaa agactgaaga aacacatctc 1200
gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc caggggtgag 1260
ggaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaacta gaaataaaca 1320
tctcaaacag taaaaaaaaa aaaaaagggc ggccgcgact ctagagtcga cctgcagaag 1380
cttggccgcc atggccaac ttgtttattg cagcttataa tgggttac 1427

```

&lt;210&gt; 153

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 153

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys  
1 5 10 15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys  
20 25 30

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly  
35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu  
50 55 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu  
65 70 75 80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu  
85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala  
100 105 110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala  
115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp  
130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys  
145 150 155 160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala  
165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr  
180 185 190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala  
195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr  
210 215 220

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg  
225 230 235 240

Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu  
245 250 255

Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val  
260 265 270

Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu  
275 280 285

Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu  
290 295 300

Arg Lys Ser Lys Asn Ser  
305 310

<210> 154

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 154

ggtgctaaac tgggtgctctg tggc

24

<210> 155

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 155

cagggcaaga tgagcattcc

20

<210> 156

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 156

tcatactgtt ccatctcggc acgc

24

<210> 157

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;400&gt; 157

aatggtggtg ccctagaaga gctcatcaga gaactcaccg cttctcatgc

50

&lt;210&gt; 158

&lt;211&gt; 1771

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 158

```

ccccgcgctc cgctggtggtt agatcgagca accctctaaa agcagtttag agtggtaaaa 60
aaaaaaaaaa acacaccaaa cgctcgagc cacaaaaggg atgaaatttc ttctggacat 120
cctcctgctt ctcccgttac tgatcgctg ctccctagag tccttcgtga agctttttat 180
tcctaagagg agaaaatcag tcaccggcga aatcggtgctg attacaggag ctgggcatgg 240
aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300
tataaataag catggactgg aggaaacagc tgccaaatgc aagggactgg gtgccaaggt 360
tcataacctt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaaggt 420
gaaggcagaa attggagatg tttagtattt agtaataaat gctggtgtag tctatacatc 480
agatttggtt gctacacaag atcctcagat tgaaaagact tttgaagtta atgtacttgc 540
acatttctgg actacaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600
tgtcactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg cttactgttc 660
aagcaagttt gctgctgttg gatttcataa aactttgaca gatgaactgg ctgccttaca 720
aataacttga gtcaaaaaca catgtctgtg tcctaatttc gtaaactctg gcttcatcaa 780
aaatccaagt acaagtttgg gaccactctt ggaacctgag gaagtggtaa acaggctgat 840
gcatgggatt ctgactgagc agaagatgat ttttattcca tcttctatag cttttttaac 900
aacattggaa aggatccttc ctgagcggtt cctggcagtt ttaaaacgaa aaatcagtgt 960
taagtttgat gcagttattg gatataaaat gaaagcgcaa taagcaccta gttttctgaa 1020
aactgattta ccaggttttag gttgatgtca tctaatagtg ccagaatttt aatgtttgaa 1080
cttctgtttt ttctaattat cccatttctt tcaatatcat ttttgaggct ttggcagttc 1140
tcatttacta ccacttgttc tttagccaaa agctgattac atatgatata aacagagaaa 1200
tacctttaga ggtgacttta aggaaaatga agaaaaagaa caaaatgac tttattaaaa 1260
taatttccaa gattatttgt ggctcacctg aaggctttgc aaaatttgta ccataaccgt 1320
ttattttaaca tatattttta tttttgattg cacttaaat tttgtataatt tgtgtttctt 1380
tttctgttct acataaaatc agaaacttca agctctctaa ataaaatgaa ggactatatc 1440
tagtggtatt tcacaatgaa tatcatgaac tctcaatggg taggtttcat cctaccatt 1500
gccactctgt ttcctgagag atacctcaca ttccaatgcc aaacatttct gcacagggaa 1560
gctagaggtg gatacacgtg ttgcaagtat aaaagcatca ctgggattta aggagaattg 1620
agagaatgta cccacaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaa 1680
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a aaaaaaaaaa 1771

```

&lt;210&gt; 159

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 159

```

Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu Leu Ile Val
 1           5           10           15
Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys
          20          25          30
Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
          35          40          45
Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val
          50          55          60
Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys
          65          70          75          80
Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn
          85          90          95

```

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly  
100 105 110  
Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp  
115 120 125  
Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn  
130 135 140  
Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr  
145 150 155 160  
Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His  
165 170 175  
Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala  
180 185 190  
Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile  
195 200 205  
Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly  
210 215 220  
Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu  
225 230 235 240  
Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met  
245 250 255  
Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile  
260 265 270  
Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys  
275 280 285  
Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln  
290 295 300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 160

ggtgaaggca gaaattggag atg

23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 161

atcccatgca tcagcctggt tacc

24

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 162  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 162  
gctggtgtag tctatacatc agatttggtt gctacacaag atcctcag 48

<210> 163  
<211> 2076  
<212> DNA  
<213> Homo sapiens

<400> 163  
cccacgcgtc cgccggacgcg tgggtcgact agttctagat cgcgagcggc cgccccgcggc 60  
tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaagggtg 120  
attgtttcgc tggtcctggt gatgcctggc ccctgtgatg ggctgtttcg ctccctatac 180  
agaagtggtt ccatgccacc taagggagac tcaggacagc cattatttct caccctttac 240  
attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggtcggccc tttcccagga 300  
ctgaacatga agagttatgc cggcttcctc accgtgaata agacttacaa cagcaacctc 360  
ttcttctggt tcttcccagc tcagatacag ccagaagatg cccagtagt tctctggcta 420  
caggggtggc cgggagggtt atccatgttt ggactctttg tggacatgg gccttatgtt 480  
gtcacaahta acatgacctt gcgtgacaga gacttcccct ggaccacaac gctctccatg 540  
ctttacattg acaatccagt gggcacaggc ttcagtttta ctgatgatac ccacggatat 600  
gcagtcaatg aggacgatgt agcacgggat ttatacagt cactaattca gtttttccag 660  
atatttcctg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcagggaaa 720  
tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780  
aacctgaacg gaattgctat tggagatgga tattctgata ccgaatcaat tatagggggc 840  
tatgcagaat tcctgtacca aattggcttg ttggatgaga agcaaaaaaa gtacttccag 900  
aagcagtgcc atgaatgcat agaacacatc aggaagcaga actgggttga ggcctttgaa 960  
atactggata aactactaga tggcgactta acaagtgatc cttcttactt ccagaatgtt 1020  
acaggatgta gtaattacta taactttttg cgggtgcacg aacctgagga tcagctttac 1080  
tatgtgaaat ttttgtcact cccagaggtg agacaagcca tccacgtggg gaatcagact 1140  
tttaattgat gaactatagt tgaaaagtac ttgcgagaag atacagtaca gtcagttaag 1200  
ccatggttaa ctgaaatcat gaataattat aaggttctga tctacaatgg ccaactggac 1260  
atcatcgtgg cagctgccct gacagagcgc tccttgatgg gcatggactg gaaaggatcc 1320  
caggaatata agaaggcaga aaaaaaagtt tggagatct ttaaatctga cagtgaagtg 1380  
gctggttaca tccggcaagc gggtgacttc catcaggtaa ttattcgagg tggaggacat 1440  
attttaccct atgaccagcc tctgagagct tttgacatga ttaatcgatt catttatgga 1500  
aaaggatggg atccttatgt tggataaaact accttcccaa aagagaacat cagaggtttt 1560  
cattgctgaa aagaaaatcg taaaaacaga aaatgtcata ggaataaaaa aattatcttt 1620  
tcatatctgc aagatttttt tcatcaataa aaattatcct tgaaacaagt gagcttttgt 1680  
ttttgggggg agatgtttac taaaaatta acatgagtac atgagtaaga attacattat 1740  
ttaacttaaa ggatgaaagg tatggatgat gtgacactga gacaagatgt ataaatgaaa 1800  
ttttagggtc ttgaatagga agttttaatt tcttctaaga gtaagtgaag agtgcagttg 1860  
taacaaacaa agctgtaaca tcttttctg ccaataacag aagtttgga tgccgtgaag 1920  
gtgttttgaa atattattgg ataagaatag ctcaattatc ccaataaaat ggatgaagct 1980  
ataatagttt tggggaaaag attctcaaat gtataaagtc ttagaacaaa agaattcttt 2040  
gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

<210> 164  
<211> 476  
<212> PRT  
<213> Homo sapiens

<400> 164  
Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met  
1 5 10 15

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser  
                   20                  25                  30  
 Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr  
                   35                  40                  45  
 Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly  
           50                  55                  60  
 Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val  
   65                  70                  75                  80  
 Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln  
                   85                  90                  95  
 Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro  
                  100                 105                 110  
 Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val  
          115                 120                 125  
 Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr  
   130                 135                 140  
 Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser  
  145                 150                 155                 160  
 Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala  
                  165                 170                 175  
 Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu  
                  180                 185                 190  
 Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys  
          195                 200                 205  
 Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg  
   210                 215                 220  
 Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser  
  225                 230                 235                 240  
 Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile  
                  245                 250                 255  
 Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His  
          260                 265  
 Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu  
   275                 280                 285  
 Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr  
  290                 295                 300  
 Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys  
  305                 310                 315                 320  
 Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro  
          325                 330                 335  
 Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly  
          340                 345                 350



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2c1.txt

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His  
435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
465 470 475

<210> 165  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 165  
ttccatgccca cctaagggag actc

24

<210> 166  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 166  
tgcatgaggt gtgcaatggc tggc

24

<210> 167  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 167  
agctctcaga ggctggtcat aggg

24

<210> 168  
<211> 50

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 168

gtcggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac

50

&lt;210&gt; 169

&lt;211&gt; 2477

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 169

cgagggcttt	tccggctccg	gaatggcaca	tgtgggaatc	ccagtcttgt	tggctacaac	60
atTTTTccct	ttcctaacaa	gttctaacag	ctgttctaac	agctagtgat	caggggttct	120
tcttgctgga	gaagaaaggg	ctgagggcag	agcagggcac	tctcactcag	ggtgaccagc	180
tccttgccctc	tctgtggata	acagagcatg	agaaagtga	gagatgcagc	ggagtgaagt	240
gatggaagtc	taaaatagga	aggaattttg	tgtgcaatat	cagactctgg	gagcagttga	300
cctggagagc	ctgggggagg	gcctgcctaa	caagctttca	aaaaacagga	gcgacttcca	360
ctgggctggg	ataagacgtg	ccggtaggat	aggggaagact	gggttttagtc	ctaatatcaa	420
attgactggc	tgggtgaact	tcaacagcct	tttaacctct	ctgggagatg	aaaacgatgg	480
cttaaggggc	cagaaataga	gatgctttgt	aaaataaaat	tttaaaaaaa	gcaagtattt	540
tatagcataa	aggctagaga	ccaaaataga	taacaggatt	ccctgaacat	tcctaagagg	600
gagaaagtat	gttaaaaata	gaaaaaccaa	aatgcagaag	gaggagactc	acagagctaa	660
accaggatgg	ggaccttggg	tcaggccagc	ctctttgctc	ctcccggaaa	ttatttttgg	720
tctgaccact	ctgccttggg	ttttgcagaa	tcattgtgag	gccaaaccgg	gaagggtggg	780
cagatgagca	cacacaggag	ccgtctcctc	accgccgccc	ctctcagcat	ggaacagagg	840
cagccctggc	cccgggccct	ggaggtggac	agccgctctg	tggtcctgct	ctcagtggtc	900
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&lt;210&gt; 170

&lt;211&gt; 552

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 170

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 1           5           10           15
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          20           25           30
Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
          35           40           45
Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
          50           55           60
Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
          65           70           75           80
Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
          85           90           95
Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
          100          105          110
Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
          115          120          125
Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
          130          135          140
Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
          145          150          155          160
Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
          165          170          175
Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys
          180          185          190
Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys
          195          200          205
Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly
          210          215          220
Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr
          225          230          235          240
Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys
          245          250          255
Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His
          260          265          270
Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala
          275          280          285
Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly
          290          295          300
Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val
          305          310          315          320
Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg

```

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
325 330 335

Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe  
340 345 350  
Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr  
355 360 365  
Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser  
370 375 380  
Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr  
385 390 395 400  
His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
405 410 415  
Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu  
420 425 430  
Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
435 440 445  
Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn  
450 455 460  
Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr  
465 470 475 480  
Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly  
485 490 495  
Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val  
500 505 510  
Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys  
515 520 525  
Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln  
530 535 540  
Leu Tyr Phe Leu Gly Glu Gln Arg  
545 550

<210> 171  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 171  
tggaataaccg cctcctgcag

20

<210> 172  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

24

<210> 173  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

43

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<210> 174
<211> 3106
<212> DNA
<213> Homo sapiens
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<220>
<221> modified_base
<222> (1683)..(1683)
<223> a, t, c or g
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<400>	174					
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tgctggctg	cttgggcttc	ctggtgctc	gcaggctga	ctggagcac	ctggtccctc	180
tgcggcttc	ccatcgacg	ctggggtgc	aggccaagg	ctggaactt	atgctggag	240
attccacct	ctggatctt	gtggggctc	tcctactatt	ccgtgtgcc	aggagtagt	300
ggagggacc	cctgtgaag	gtgaaggcct	gtggcttgaa	caccttcacc	acctatgtt	360
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tgatgtccag	ggtgtgtcca	ctccagttaca	agcgtggggg	acctatcatt	gccgtgcagg	660
tggagaatga	atatggttcc	tataataaag	acccgcata	catgccctac	gtcaagaagg	720
cactggagga	ccgtggcatt	gtggaactgc	tcctgacttc	agacaacaag	gatgggctga	780
gcaaggggat	tgtccaggga	gtcttgcca	ccatcaactt	gcagtcaaca	cacgagctgc	840
agctactgac	cacctttctc	ttcaacgtcc	aggggactca	gcccagaagt	gtgatggagt	900
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gccctgcatt	acagttcacg	gaaaccccc	acctgggcag	gaaccagtac	attaagtgag	1980
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2c1.txt

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<210> 175  
 <211> 636  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MOD\_RES  
 <222> (539)  
 <223> Any amino acid

<400> 175  
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 20 25 30  
 Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln  
 35 40 45  
 Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe  
 50 55 60  
 Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp  
 65 70 75 80  
 Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr  
 85 90 95  
 Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser  
 100 105 110  
 Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly  
 115 120 125  
 Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp  
 130 135 140  
 Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu  
 145 150 155 160  
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp  
 165 170 175

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro  
 180 185 190  
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp  
 195 200 205  
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile  
 210 215 220  
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly  
 225 230 235 240  
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu  
 245 250 255  
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro  
 260 265 270  
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly  
 275 280 285  
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala  
 290 295 300  
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly  
 305 310 315 320  
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys  
 325 330 335  
 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly  
 340 345 350  
 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile  
 355 360 365  
 Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys Met Pro  
 370 375 380  
 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu  
 385 390 395 400  
 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu  
 405 410 415  
 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu  
 420 425 430  
 Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
 435 440 445  
 Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
 450 455 460  
 Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val  
 465 470 475 480  
 Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn  
 485 490 495  
 Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp  
 500 505 510

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser  
515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr  
530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr  
545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val  
565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln  
580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln  
595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr  
610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys  
625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

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aaggggagca aagccgggct cggcccaggc cccccaggac ctccatctcc caatgttga 180
ggaatccgac acgtgacggg ctgtccgccc tctcagacta gaggagcgct gtaaaccgca 240
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actccaaaac atttccaatt ttaggctcag ttggggacac atttctatat ctacctggat 1920
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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2c1.txt

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agcctatcct caatagcact agtactttgc acaggacaca tatcaattcc ctttcagctg 2160
atacactgag tgcctctgaa ccaatggagt taagtgggca ctgaaaggta ggccgggcat 2220
ggtggctcat gcctgtaatc ccagcacttt gggaggctga gacgggtgga ttacctgagg 2280
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ggagaattgc ttgaatccag gaggcagagg ttgcagtgag tggagggtgt accactgcac 2460
tccagcctgg ctgacagtga gacactccat ctcaaaaaaa aaaaaa 2505

```

&lt;210&gt; 177

&lt;211&gt; 654

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 177

```

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Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val
          20          25          30
Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
          35          40          45
Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
          50          55          60
Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe
          65          70          75          80
Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe
          85          90          95
Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala
          100          105          110
Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp
          115          120          125
Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His
          130          135          140
Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe
          145          150          155          160
Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly
          165          170          175
Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala
          180          185          190
Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu
          195          200          205
Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu
          210          215          220
Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro
          225          230          235          240
Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro
          245          250          255

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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr  
 260 265 270  
 Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly  
 275 280 285  
 Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe  
 290 295 300  
 His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly  
 305 310 315 320  
 Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser  
 325 330 335  
 Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile  
 340 345 350  
 Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro  
 355 360 365  
 Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu  
 370 375 380  
 Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu  
 385 390 395 400  
 Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr  
 405 410 415  
 Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val  
 420 425 430  
 Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val  
 435 440 445  
 Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr  
 450 455 460  
 Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg  
 465 470 475 480  
 Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro  
 485 490 495  
 Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu  
 500 505 510  
 Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys  
 515 520 525  
 Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr  
 530 535 540  
 Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly  
 545 550 555 560  
 Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr  
 565 570 575  
 Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu  
 580 585 590

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu  
 595 600 605  
 Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu  
 610 615 620  
 Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala  
 625 630 635 640  
 Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His  
 645 650

<210> 178  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 178  
 tggctactcc aagaccctgg catg 24

<210> 179  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 179  
 tggacaaatc cccttgctca gccc 24

<210> 180  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 180  
 gggcttcacc gaagcagtgg acctttatatt tgaccacctg atgtccaggg 50

<210> 181  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 181  
 ccagctatga ctatgatgca cc 22

<210> 182  
 <211> 24

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 182

tggcaccag aatggtgttg gctc

24

<210> 183

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 183

cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc

50

<210> 184

<211> 1947

<212> DNA

<213> Homo sapiens

<400> 184

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gtgtttatgg ctttatctgc ctctacactc tcttctgggt attcaggata cctttgaagg 180
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acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagcgtt 300
ttggtgtgtt cttgtcagaa gttagtgaat ataaacttag ggaaattagt ttgaaccatg 360
agtggacatt tgaaaaactc aggcagcaca tttcacgcaa cgcccaggac aagcaggagt 420
tgcatctgtt catgctgtcg ggggtgcccg atgctgtctt tgacctcaca gacctggatg 480
tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540
acctccaaga gctccacctc tgccactgcc ctgcaaaaagt tgaacagact gcttttagct 600
tcttctcgca tcacttgaga tgccttcacg tgaagttcac tgatgtggct gaaattcctg 660
ttcgggtgta tttgtcctaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720
aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780
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aggggaaggaa aaattataat cactaatctt ggttcttttt aaattgtttg taacttggat 1860
gctgccgcta ctgaatgttt acaaatgtct tgcctgctaa agtaaatgat taaattgaca 1920
ttttcttact aaaaaaaaaa aaaaaaa 1947

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<210> 185

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;211&gt; 501

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 185

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Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile
 1          5          10          15
Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg
          20          25          30
Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser
          35          40          45
Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His
          50          55          60
Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe
 65          70          75          80
Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His
          85          90          95
Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln
          100          105          110
Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala
          115          120          125
Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro
          130          135          140
Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu
145          150          155          160
Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser
          165          170          175
Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val
          180          185          190
Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu
          195          200          205
Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu
210          215          220
Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser
225          230          235          240
Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu
          245          250          255
Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn
          260          265          270
Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys
          275          280          285
Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln
290          295          300
Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

305                    310                    315                    320  
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                          325                    330                    335  
 Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu  
                          340                    345                    350  
 Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val  
                          355                    360                    365  
 Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile  
                          370                    375                    380  
 Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu  
                          385                    390                    395                    400  
 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys  
                          405                    410                    415  
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser  
                          420                    425                    430  
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu  
                          435                    440                    445  
 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg  
                          450                    455                    460  
 Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr  
                          465                    470                    475                    480  
 Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro  
                          485                    490                    495  
 Phe Ala Asn Gly Ile  
                          500

<210> 186  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 186  
 cctccctcta ttacccatgt c

21

<210> 187  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 187  
 gaccaacttt ctctgggagt gagg

24

<210> 188

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;211&gt; 47

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic oligonucleotide probe

&lt;400&gt; 188

gtcactttat ttctctaaca acaagctcga atccttacca gtggcag

47

&lt;210&gt; 189

&lt;211&gt; 2917

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 189

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cccacgcgtc cggcctttctc tctggacttt gcattttccat tcctttttcat tgacaaaactg 60
acttttttta tttctttttt tccatctctg ggccagcttg ggatcctagg ccgccctggg 120
aagacatttg tgttttacac acataaggat ctgtgttttg ggtttcttct tcctcccctg 180
acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240
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cacaacccag acaaggtgtg gtgggccaag aacagccagg ccaaaccat tgccacggag 480
tcttgtcctg ccctgcagtg ctgtgaagga tatagaatgt gtgccagttt tgattccctg 540
ccaccttgct gttgcgacat aaatgagggc ctctgagtta ggaaaggctc ctttctcaaa 600
gcagagccct gaagacttca atgatgtcaa tgaggccacc tgtttgtgat gtgcaggcac 660
agaagaaagg cacagctccc catcagtttc atggaaaata actcagtgcc tgctgggaac 720
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gaaactccaa accagccttt caacagtgtg catctgtttt cttcatggg tctagctctg 2700
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
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 tccaggatgc caaaggaaat gctacctcgt ggctacacat attatgaata aatgaggaag 2880  
 ggcctgaaag tgacacacag gcctgcatgt aaaaaaa 2917

<210> 190  
 <211> 607  
 <212> PRT  
 <213> Homo sapiens

<400> 190  
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 Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys  
 20 25 30  
 Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met  
 35 40 45  
 Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg  
 50 55 60  
 Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp  
 65 70 75 80  
 Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr  
 85 90 95  
 Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr  
 100 105 110  
 Val Pro Val Phe Glu Ser Ser Ser Thr Leu Thr Phe Gln Ile Val  
 115 120 125  
 Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe  
 130 135 140  
 Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr  
 145 150 155 160  
 Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu  
 165 170 175  
 Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile  
 180 185 190  
 Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys  
 195 200 205  
 Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu  
 210 215 220  
 Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser  
 225 230 235 240  
 Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg  
 245 250 255  
 Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr  
 260 265 270  
 Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys  
 275 280 285



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02p1618P2C1.txt

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys  
290 295 300

Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val  
305 310 315 320

Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile  
325 330 335

Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val  
340 345 350

Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly  
355 360 365

His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile  
370 375 380

Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe  
385 390 395 400

Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val  
405 410 415

Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp  
420 425 430

Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser  
435 440 445

Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg  
450 455 460

Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe  
465 470 475 480

Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu  
485 490 495

Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys  
500 505 510

Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys  
515 520 525

Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg  
530 535 540

Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu  
545 550 555 560

Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val  
565 570 575

Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe  
580 585 590

Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr  
595 600 605

<210> 191

<211> 21

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2c1.txt

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic oligonucleotide probe

&lt;400&gt; 191

tctctattcc aaactgtggc g

21

&lt;210&gt; 192

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic oligonucleotide probe

&lt;400&gt; 192

tttgatgacg attcgaaggt gg

22

&lt;210&gt; 193

&lt;211&gt; 47

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic oligonucleotide probe

&lt;400&gt; 193

ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc

47

&lt;210&gt; 194

&lt;211&gt; 2362

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 194

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cgggacatgc	ggccccagga	gctccccagg	ctcgcgttcc	cgttgctgct	gttgctgttg	120
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cccacactag	atggcaccat	ttctgtagtt	tttgaggagc	gactgaggca	agtgggggtc	1140
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actgtcaccc	cagatgtgtg	gtacacatcc	aagcctaaag	aaaaattagt	ctatgccatt	1260
tttcttaaat	ggcccacatc	aggacagctg	ttccttggcc	atcccaaagc	tattctgggg	1320
gcaacagagg	tgaaactact	gggccatgga	cagccactta	actggatttc	tttgagcaaa	1380

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

```

aatggcatta tggtagaact gccacagcta accattcatc agatgccgtg taaatggggc 1440
tgggctctag ccctaactaa tgtgatctaa agtgcagcag agtggctgat gctgcaagtt 1500
atgtctaagg ctaggaacta tcaggtgtct ataattgtag cacatggaga aagcaatgta 1560
aactggataa gaaaattatt tggcagttca gccctttccc tttttccac taaatttttc 1620
ttaaattacc catgtaacca ttttaactct ccagtgcaact ttgccattaa agtctcttca 1680
cattgatttg tttccatgtg tgactcagag gtgagaattt tttcacatta tagtagcaag 1740
gaattgggtg tattatggac cgaactgaaa attttatgtt gaagccatat ccccatgat 1800
tatatagtta tgcatactt aatatgggga tttttctgg gaaatgcatt gctagtcaat 1860
ttttttttgt gccaacatca tagagtgtat ttacaaaatc ctagatggca tagcctacta 1920
cacacctaat gtgtatggta tagactgttg ctcttaggct acagacatat acagcatgtt 1980
actgaatact gtaggcaata gtaacagtgg tattttgtata tcgaaacata tggaaacata 2040
gagaaggtag agtaaaaaata ctgtaaaaata aatgggtgcac ctgtataggg cacttaccac 2100
gaatggagct tacaggactg gaagttgctc tgggtgagtc agtgagtga tgtgaaggcc 2160
taggacatta ttgaacactg ccagacgtta taaatactgt atgcttaggc tacactacat 2220
ttataaaaaa aagtttttct ttcttcaatt ataaattaac ataagtgtac tgtaacttta 2280
caaacgtttt aatttttaaa acctttttgg ctcttttgta ataacactta gcttaaaaca 2340
taaactcatt gtgcaaatgt aa 2362

```

&lt;210&gt; 195

&lt;211&gt; 467

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 195

```

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu
 1           5           10           15

```

```

Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr
 20           25           30

```

```

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
 35           40           45

```

```

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe
 50           55           60

```

```

Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys
 65           70           75           80

```

```

Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro
 85           90           95

```

```

Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe
100           105           110

```

```

Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr
115           120           125

```

```

Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser
130           135           140

```

```

Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp
145           150           155           160

```

```

Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg
165           170           175

```

```

Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu
180           185           190

```

```

Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys
195           200           205

```

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val  
 210 215 220

Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser  
 225 230 235 240

Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr  
 245 250 255

Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly  
 260 265 270

Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro  
 275 280 285

His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr  
 290 295 300

Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val  
 305 310 315 320

Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn  
 325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg  
 340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr  
 355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val  
 370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu  
 385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile  
 405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn  
 420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu  
 435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr  
 450 455 460

Asn Val Ile  
 465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 196

tggtttgacc aggccaagtt cgg

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 197  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 197  
 ggattcatcc tcaaggaaga gcgg 24

<210> 198  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 198  
 aacttgacgc atcagccact ctgc 24

<210> 199  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 199  
 ttccgtgccc agcttcggta gcgagtgggt ctgggtggat tggca 45

<210> 200  
 <211> 2372  
 <212> DNA  
 <213> Homo sapiens

<400> 200  
 agcagggaag tccggatgtc tcgggttatga agtggagcag tgagtgtgag cctcaacata 60  
 gttccagaac tctccatccg gactagttat tgagcatctg cctctcatat caccagtggc 120  
 catctgaggt gtttccctgg ctctgaaggg gtaggcacga tggccagggtg cttcagcctg 180  
 gtgtgtcttc tcacttccat ctggaccacg aggtctcctg tccaaggctc tttgcgtgca 240  
 gaagagcttt ccatccagggt gtcattgcaga attatgggga tcacccttgt gagcaaaaag 300  
 gcgaaccagc agctgaattt cacagaagct aaggaggcct gtaggctgct gggactaagt 360  
 ttggccggca aggaccaagt tgaaacagcc ttgaaagcta gctttgaaac ttgcagctat 420  
 ggctggggtg gagatggatt cgtgggtcatc tctaggatta gcccaaacc caagtgtggg 480  
 aaaaatgggg tgggtgtcct gatttggaag gttccagtga gccgacagtt tgcagcctat 540  
 tgttacaact catctgatac ttggactaac tcgtgcattc cagaaattat caccaccaa 600  
 gatcccatat tcaacactca aactgcaaca caaacaacag aatttattgt cagtgcacag 660  
 acctactcgg tggcatcccc ttactctaca atacctgccc ctactactac tcctcctgct 720  
 ccagcttcca ctctatttcc acggagaaaa aaattgattt gtgtcacaga agtttttatg 780  
 gaaactagca ccatgtctac agaaactgaa ccatgtgttg aaaataaagc agcattcaag 840  
 aatgaagctg ctgggttttg aggtgtcccc acggctctgc tagtgcttgc tctcctcttc 900  
 tttggtgctg cagctgggtc ttgattttgc tatgtcaaaa ggtatgtgaa ggccttccct 960  
 tttcaaaaaa agaatacaga gaaggaaatg atcgaaacca aagtagtaaa ggaggagaag 1020  
 gccaatgata gcaaccctaa tgaggaaatc aagaaaactg ataaaaacc agaagagtcc 1080  
 aagagtccaa gcaaaactac cgtgcgatgc ctggaagctg aagtttagat gagacagaaa 1140  
 tgaggagaca cacctgaggc tggtttcttt catgtcctt accctgcccc agctggggaa 1200  
 atcaaaaagg ccaaagaacc aaagaagaaa gtccaccctt ggttcctaac tggaatcagc 1260

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

```

tcaggactgc cattggacta tggagtgcac caaagagaat gcccttctcc ttattgtaac 1320
cctgtctgga tcctatcctc ctacctccaa agcttcccac ggcctttcta gcctggctat 1380
gtcctaataa tatccactg ggagaaagga gttttgcaa gtgcaaggac ctaaaacatc 1440
tcatcagtat ccagtggtaa aaaggcctcc tggctgtctg aggctagggt ggttgaaagc 1500
caaggagtca ctgagaccaa ggctttctct actgattccg cagctcagac cttttcttca 1560
gctctgaaag agaaacacgt atcccactg acatgtcctt ctgagcccgg taagagcaaa 1620
agaatggcag aaaagttag cccctgaaag ccatggagat tctcataact tgagacctaa 1680
tctctgtaaa gctaaaataa agaaatagaa caaggctgag gatacgacag tacactgtca 1740
gcagggactg taaacacaga cagggtcaaa gtgttttctc tgaacacatt gagttggaat 1800
cactgtttag aacacacaca ctacttttt ctggtctcta ccactgctga tattttctct 1860
aggaaatata cttttacaag taacaaaaat aaaaactctt ataaatttct atttttatct 1920
gagttacaga aatgattact aaggaagatt actcagtaat ttgtttaaaa agtaataaaa 1980
ttcaacaaac atttgctgaa tagctactat atgtcaagtg ctgtgcaagg tattacactc 2040
tgtaattgaa tattattcct caaaaaattg cacatagtag aacgctatct gggaagctat 2100
ttttttcagt tttgatattt ctagcttatc tacttccaaa ctaattttta tttttgctga 2160
gactaatctt attcattttc tctaattatg taaccattat aaccttaatt tattattaac 2220
atacctaaga agtacattgt tacctctata taccaaagca cattttaaaa gtgccattaa 2280
caaatgtatc actagccctc ctttttccaa caagaagggg ctgagagatg cagaaatatt 2340
tgtgacaaaa aattaaagca tttagaaaac tt 2372

```

<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr  
1 5 10 15

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile  
20 25 30

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala  
35 40 45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu  
50 55 60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala  
65 70 75 80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val  
85 90 95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly  
100 105 110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys  
115 120 125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile  
130 135 140

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
145 150 155 160

Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
165 170 175

Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

180 185 190  
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
 195 200 205  
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
 210 215 220  
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu  
 225 230 235 240  
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
 245 250 255  
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
 260 265 270  
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
 275 280 285  
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro  
 290 295 300  
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala  
 305 310 315 320  
 Glu Val

<210> 202  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 202  
 gagctttcca tccaggtgtc atgc 24

<210> 203  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 203  
 gtcagtga gacactac gg 22

<210> 204  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 204

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

tggagcagga ggagtagtag tagg

24

&lt;210&gt; 205

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 205

aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt

50

&lt;210&gt; 206

&lt;211&gt; 1620

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; modified\_base

&lt;222&gt; (973)..(973)

&lt;223&gt; a, t, c or g

&lt;220&gt;

&lt;221&gt; modified\_base

&lt;222&gt; (977)..(977)

&lt;223&gt; a, t, c or g

&lt;220&gt;

&lt;221&gt; modified\_base

&lt;222&gt; (996)..(996)

&lt;223&gt; a, t, c or g

&lt;220&gt;

&lt;221&gt; modified\_base

&lt;222&gt; (1003)..(1003)

&lt;223&gt; a, t, c or g

&lt;400&gt; 206

```

agatggcggg cttggcacct ctaattgctc tcgtgtattc ggtgccgcga ctttcacgat 60
ggctcgccca accttactac cttctgtcgg ccctgctctc tgctgccttc ctactcgtga 120
ggaaactgcc gccgctctgc cacggtctgc ccacccaacg cgaagacggg aaccctgtgt 180
actttgactg gagagaagtg gagatcctga tgtttctcag tgccattgtg atgatgaaga 240
accgcagatc catcactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300
ccaacacaat tcttttcttc cgcttgataa ttcgcatggg cctactttac atcacactct 360
gcatagtgtt cctgatgacg tgcaaaccct ccctatatat gggccctgag tatatcaagt 420
acttcaatga taaaaccatt gatgaggaac tagaacggga caagagggtc acttggattg 480
tggagtctct tgccaattgg tctaattgact gccaatcatt tgcccctatc tatgctgacc 540
tctcccttaa atacaactgt acagggctaa attttgggaa ggtggatgtt ggacgctata 600
ctgatgttag tacgcggtac aaagttagca catcaccctt caccaagcaa ctccctacct 660
tgatcctgtt ccaagggtggc aaggaggcaa tgcggcgggc acagattgac aagaaaggac 720
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gctgcagcct ttnattnatg ttttcccttt ggctgngact ggntggggca gcatgcagct 1020
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tgtggccaac tgtttcactg gagcaagaaa gagatctcat aggacggagg gggaaatggg 1140
ttccctccaa gcttgggtca gtgtgttaac tgcttatcag ctattcagac atctccatgg 1200
tttctccatg aaactctgtg gtttcatcat tccttcttag ttgacctgca cagcttgggt 1260
agacctagat ttaaccctaa ggtaagatgc tggggtatag aacgctaaga attttcccc 1320
aaggactctt gcttccttaa gcccttctgg cttcgtttat ggtcttcatt aaaagtataa 1380

```



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

gcctaacttt gtcgctagtc ctaaggagaa acccttaacc acaaagtttt tatcattgaa 1440  
gacaatattg aacaaccccc tattttgtgg ggattgagaa ggggtgaata gaggcttgag 1500  
actttccttt gtgtggtagg acttggagga gaaatcccct ggactttcac taaccctctg 1560  
acatactccc cacaccagtg tgatggcttt ccgtaataaa aagattggga tttccttttg 1620

<210> 207

<211> 296

<212> PRT

<213> Homo sapiens

<400> 207

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg  
1 5 10 15  
Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu  
20 25 30  
Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly  
35 40 45  
Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg  
50 55 60  
Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn  
65 70 75 80  
Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
85 90 95  
Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
100 105 110  
Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
115 120 125  
Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys  
130 135 140  
Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val  
145 150 155 160  
Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile  
165 170 175  
Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly  
180 185 190  
Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val  
195 200 205  
Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln  
210 215 220  
Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg  
225 230 235 240  
Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn  
245 250 255  
Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp  
260 265 270  
Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser

Asp Gly Glu Asn Lys Lys Asp Lys  
290 295

<210> 208  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 208  
gcttgatat tcgcatgggc ctac 24

<210> 209  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 209  
tggagacaat atccctgagg 20

<210> 210  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 210  
aacagttggc cacagcatgg cagg 24

<210> 211  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 211  
ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212  
<211> 1985  
<212> DNA  
<213> Homo sapiens

<400> 212  
ggacagctcg cggcccccca gagctctagc cgctcaggag ctgcctgggg acgtttgccc 60  
tggggcccca gcctggcccc ggtcaccctg gcatgaggag atgggcctgt tgctcctggg 120  
cccattgctc ctgctgcccc gctcctacgg actgcccttc tacaacggct tctactactc 180  
caacagcgcc aacgaccaga acctaggcaa cggtcatggc aaagacctcc ttaatggagt 240

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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gaagctggtg gtggagacac ccgaggagac cctgttcacc taccaagggg ccagtgtgat 300
cctgcccctgc cgctaccgct acgagccggc cctgggtctcc ccgcggcgtg tgcgtgtcaa 360
atggtggaag ctgtcggaga acggggcccc agagaaggac gtgctggtgg ccacgggct 420
gaggcaccgc tcctttgggg actaccaagg ccgctgtcac ctgcccaggg acaaagagca 480
tgacgtctcg ctggagatcc aggatctgcg gctggaggac tatgggcgtt accgctgtga 540
ggtcattgac gggctggagg atgaaagcgg tctgggtggag ctggagctgc ggggtgtggt 600
ctttccttac cagtcccca acgggcgcta ccagttcaac ttccacgagg gccagcaggt 660
ctgtgcagag caggctgcgg tgggtggcctc ctttgagcag ctcttcggg cctgggagga 720
gggcctggac tgggtgcaacg cgggctggct gcaggatgct acggtgcagt accccatcat 780
gttgcccccg cagccctgcg gtggcccagg cctggcacct ggctgtcgaa gctacggccc 840
ccgccaccgc cgcctgcacc gctatgatgt attctgcttc gctactgccc tcaaggggag 900
ggtgtactac ctggagcacc ctgagaagct gacgtgaca gaggcaaggg aggcctgcca 960
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cccgcatcct aactgtgggc ccccagagcc tggggctcca agctttggct tccccgacct 1140
gcagagccgc ttgtacggtg tttactgcta ccgccagcac taggacctgg ggccctcccc 1200
tgccgcattc cctcactggc tgtgtattta ttgagtgggt cgttttccct tgtgggttgg 1260
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agaatgccgc cgggagtcgg ggcatggtgg gcacagttct ccctgcccct cagcctgggg 1560
gaagaagagg gcctcggggg cctccggagc tgggctttgg gcctctcctg cccacctcta 1620
cttctctgtg aagccgctga cccagctctg cccactgagg ggctagggct ggaagccagt 1680
tctaggcttc caggcgaat ctgagggaag gaagaaactc ccctccccgt tccccttccc 1740
ctctcggttc caaagaatct gttttgttgt catttgtttc tcctgtttcc ctgtgtgggg 1800
aggggcccctc aggtgtgtgt actttggaca ataaatggtg ctatgactgc cttccgcaa 1860
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
aaaaaa

```

&lt;210&gt; 213

&lt;211&gt; 360

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 213

```

Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Pro Gly Ser Tyr
  1             5             10             15
Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
             20             25             30
Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
             35             40             45
Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
             50             55             60
Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
             65             70             75             80
Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
             85             90             95
Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe
             100            105            110
Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp
             115            120            125
Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr
             130            135            140

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu  
145 150 155 160  
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg  
165 170 175  
Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala  
180 185 190  
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly  
195 200 205  
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr  
210 215 220  
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro  
225 230 235 240  
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp  
245 250 255  
Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu  
260 265 270  
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu  
275 280 285  
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys  
290 295 300  
Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser  
305 310 315 320  
Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu  
325 330 335  
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr  
340 345 350  
Gly Val Tyr Cys Tyr Arg Gln His  
355 360

<210> 214

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 214

tgcttcgcta ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 215  
ttcccttggtg ggttgag 18

<210> 216  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 216  
agggctggaa gccagttc 18

<210> 217  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 217  
agccagtggag gaaatgag 18

<210> 218  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 218  
tgtccaaagt acacacacct gagg 24

<210> 219  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 219  
gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag 45

<210> 220  
<211> 1503  
<212> DNA  
<213> Homo sapiens

<400> 220  
ggagagcgga gcgaagctgg ataacagggg accgatgatg tggcgaccat cagttctgct 60  
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tggccagggg aggggtgcacc aggcggcccc cctgagcgac gctccccatg atgacgcca 180  
cgggaaacttc cagtacgacc atgaggcttt cctgggacgg gaagtggcca aggaattcga 240  
ccaactcacc ccagaggaaa gccaggcccg tctggggcgg atcgtggacc gcatggaccg 300

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2c1.txt

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cgcggggggac ggcgacggct ggggtgtcgt ggccgagctt cgcgcggtgga tcgcgcacac 360
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cgacgggctgt gtgggttggg aggagctgag caacgccacc tatggccact acgcgcccgg 480
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ggaggacctg gacagaaaca aagatggcta tgtccagggtg gaggagtaca tcgcggtatct 720
gtactcagcc gagcctgggg aggaggagcc ggcgtgggtg cagacggaga ggcagcagtt 780
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aaa 1503

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<210> 221  
 <211> 328  
 <212> PRT  
 <213> Homo sapiens

<400> 221  
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 Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala  
 35 40 45  
 His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val  
 50 55 60  
 Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu  
 65 70 75 80  
 Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp  
 85 90 95  
 Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg  
 100 105 110  
 His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp  
 115 120 125  
 Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly  
 130 135 140  
 His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr  
 145 150 155 160  
 Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp  
 165 170 175  
 Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu  
 180 185 190

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr  
195 200 205  
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu  
210 215 220  
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala  
225 230 235 240  
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn  
245 250 255  
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro  
260 265 270  
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu  
275 280 285  
Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
290 295 300  
Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
305 310 315 320  
Leu Thr Arg His His Asp Glu Leu  
325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 225  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 225  
ccccctgag cgacgctccc ccatgatgac gccacggga actt 44

<210> 226  
<211> 2403  
<212> DNA  
<213> Homo sapiens

<400> 226  
ggggccttgc cttccgcact cgggcgagc cgggtggatc tcgagcaggt gaggagcccc 60  
gggcgggcgg cgcggtgctg agggatccct gacgcctctg tccctgttct ttgtcgctc 120  
ccagcctgtc tgctcgctgt ttggcgcccc cgctccccg cgggtcgggg ttgcacaccg 180  
atcctgggct tcgctcgatt tgccgcccag gcgcctccca gacctagagg ggcgctggcc 240  
tggagcagcg ggtcgtctgt gtctctctct ctctgcgcg cggccgggga tccgaagggt 300  
gcggggctct gaggaggtga cgcgcggggc ctcccgacc ctggccttgc ccgcattctc 360  
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cacatgatgc aggaatcact atcttctctg ttggtgtggc ttgggcacct ctggatgacc 1920  
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gattagaacc aattgtttct gatgtcatca gaggcatttg tagagatttc ttagaatccc 2040  
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attgtattct cataatactg aaatgcttta gcatactaga atcagatata aaactattaa 2160  
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aaa 2403

<210> 227  
<211> 550



## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 227

Met Ser Ala Ala Trp Ile Pro Ala Leu Gly Leu Gly Val Cys Leu Leu  
 1 5 10 15  
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 20 25 30  
 Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val  
 35 40 45  
 Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn  
 50 55 60  
 Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg  
 65 70 75 80  
 Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro  
 85 90 95  
 Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln  
 100 105 110  
 Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser  
 115 120 125  
 Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro  
 130 135 140  
 Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys  
 145 150 155 160  
 Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile  
 165 170 175  
 Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala  
 180 185 190  
 Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln  
 195 200 205  
 Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser  
 210 215 220  
 Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly  
 225 230 235 240  
 Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe  
 245 250 255  
 Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val  
 260 265 270  
 Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val  
 275 280 285  
 Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro  
 290 295 300  
 Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys  
 305 310 315 320

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp  
325 330 335

Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr  
340 345 350

His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile  
355 360 365

Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg  
370 375 380

Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser  
385 390 395 400

Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg  
405 410 415

Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala  
420 425 430

Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp  
435 440 445

Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser  
450 455 460

Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp  
465 470 475 480

Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile  
485 490 495

Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met  
500 505 510

Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr  
515 520 525

Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp  
530 535 540

Phe Leu Glu Ser Gln Gln  
545 550

<210> 228

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 228

tggtctcgca caccgatc

18

<210> 229

<211> 18

<212> DNA

<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2c1.txt

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 229  
 ctgctgtcca caggggag 18

<210> 230  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 230  
 ccttgaagca tactgctc 18

<210> 231  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 231  
 gagatagcaa tttccgcc 18

<210> 232  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 232  
 ttcctcaaga gggcagcc 18

<210> 233  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 233  
 cttggcacca atgtccgaga tttc 24

<210> 234  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 234  
gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg

45

<210> 235  
<211> 2586  
<212> DNA  
<213> Homo sapiens

<400> 235  
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ccggcggcct cccggcggga gcgagcagat ccagtccggc ccgcagcgca actcgggtcca 120  
gtcggggcgg cggtgcggg gcgagagcgg agatgcagcg gcttggggcc accctgctgt 180  
gcctgctgct ggcggcggcg gtccccacgg ccccgcgcc cgctccgacg gcgacctcgg 240  
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tggtccgcga ggttgaggaa ctgatggagg acacgcagca caaattgcgc agcgcggtgg 360  
aagagatgga ggagaaagaa gctgctgcta aagcatcatc agaagtgaac ctggcaaaact 420  
tacctccag ctatcacaat gagaccaaca cagacacgaa ggttggaat aataccatcc 480  
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tgatgttttc aggtgtcatg gactgttgcc accatgtatt catccagagt tcttaaagtt 2460  
taaagttgca catgattgta taagcatgct ttctttgagt tttaaattat gtataaacat 2520  
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aaaaaa 2586

<210> 236  
<211> 350  
<212> PRT  
<213> Homo sapiens

<400> 236  
Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala  
1 5 10 15

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val  
20 25 30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn  
35 40 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys  
50 55 60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys  
65 70 75 80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn  
85 90 95

Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His  
100 105 110

Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe  
115 120 125

Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser  
130 135 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln  
145 150 155 160

Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met  
165 170 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp  
180 185 190

Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys  
195 200 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
210 215 220

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
225 230 235 240

Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu  
245 250 255

Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe  
275 280 285

Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val  
290 295 300

Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu  
305 310 315 320

Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu  
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Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 <212> PRT  
 <213> Homo Sapien

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 Ser Tyr Arg Glu Ala Thr Thr Val Asp Cys Asn Asp Leu Phe Leu  
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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu	110	115	120
Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His	125	130	135
Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His	140	145	150
Asn	Gln	Leu	Tyr	Arg	Ile	Ala	Pro	Arg	Ala	Phe	Ser	Gly	Leu	Ser	155	160	165
Asn	Leu	Leu	Arg	Leu	His	Leu	Asn	Ser	Asn	Leu	Leu	Arg	Ala	Ile	170	175	180
Asp	Ser	Arg	Trp	Phe	Glu	Met	Leu	Pro	Asn	Leu	Glu	Ile	Leu	Met	185	190	195
Ile	Gly	Gly	Asn	Lys	Val	Asp	Ala	Ile	Leu	Asp	Met	Asn	Phe	Arg	200	205	210
Pro	Leu	Ala	Asn	Leu	Arg	Ser	Leu	Val	Leu	Ala	Gly	Met	Asn	Leu	215	220	225
Arg	Glu	Ile	Ser	Asp	Tyr	Ala	Leu	Glu	Gly	Leu	Gln	Ser	Leu	Glu	230	235	240
Ser	Leu	Ser	Phe	Tyr	Asp	Asn	Gln	Leu	Ala	Arg	Val	Pro	Arg	Arg	245	250	255
Ala	Leu	Glu	Gln	Val	Pro	Gly	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys	260	265	270
Asn	Pro	Leu	Gln	Arg	Val	Gly	Pro	Gly	Asp	Phe	Ala	Asn	Met	Leu	275	280	285
His	Leu	Lys	Glu	Leu	Gly	Leu	Asn	Asn	Met	Glu	Glu	Leu	Val	Ser	290	295	300
Ile	Asp	Lys	Phe	Ala	Leu	Val	Asn	Leu	Pro	Glu	Leu	Thr	Lys	Leu	305	310	315
Asp	Ile	Thr	Asn	Asn	Pro	Arg	Leu	Ser	Phe	Ile	His	Pro	Arg	Ala	320	325	330
Phe	His	His	Leu	Pro	Gln	Met	Glu	Thr	Leu	Met	Leu	Asn	Asn	Asn	335	340	345
Ala	Leu	Ser	Ala	Leu	His	Gln	Gln	Thr	Val	Glu	Ser	Leu	Pro	Asn	350	355	360
Leu	Gln	Glu	Val	Gly	Leu	His	Gly	Asn	Pro	Ile	Arg	Cys	Asp	Cys	365	370	375
Val	Ile	Arg	Trp	Ala	Asn	Ala	Thr	Gly	Thr	Arg	Val	Arg	Phe	Ile	380	385	390

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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Leu	Pro	Val	Arg	Glu	Val	Pro	Phe	Arg	Glu	Met	Thr	Asp	His	Cys
				410					415					420
Leu	Pro	Leu	Ile	Ser	Pro	Arg	Ser	Phe	Pro	Pro	Ser	Leu	Gln	Val
				425					430					435
Ala	Ser	Gly	Glu	Ser	Met	Val	Leu	His	Cys	Arg	Ala	Leu	Ala	Glu
				440					445					450
Pro	Glu	Pro	Glu	Ile	Tyr	Trp	Val	Thr	Pro	Ala	Gly	Leu	Arg	Leu
				455					460					465
Thr	Pro	Ala	His	Ala	Gly	Arg	Arg	Tyr	Arg	Val	Tyr	Pro	Glu	Gly
				470					475					480
Thr	Leu	Glu	Leu	Arg	Arg	Val	Thr	Ala	Glu	Glu	Ala	Gly	Leu	Tyr
				485					490					495
Thr	Cys	Val	Ala	Gln	Asn	Leu	Val	Gly	Ala	Asp	Thr	Lys	Thr	Val
				500					505					510
Ser	Val	Val	Val	Gly	Arg	Ala	Leu	Leu	Gln	Pro	Gly	Arg	Asp	Glu
				515					520					525
Gly	Gln	Gly	Leu	Glu	Leu	Arg	Val	Gln	Glu	Thr	His	Pro	Tyr	His
				530					535					540
Ile	Leu	Leu	Ser	Trp	Val	Thr	Pro	Pro	Asn	Thr	Val	Ser	Thr	Asn
				545					550					555
Leu	Thr	Trp	Ser	Ser	Ala	Ser	Ser	Leu	Arg	Gly	Gln	Gly	Ala	Thr
				560					565					570
Ala	Leu	Ala	Arg	Leu	Pro	Arg	Gly	Thr	His	Ser	Tyr	Asn	Ile	Thr
				575					580					585
Arg	Leu	Leu	Gln	Ala	Thr	Glu	Tyr	Trp	Ala	Cys	Leu	Gln	Val	Ala
				590					595					600
Phe	Ala	Asp	Ala	His	Thr	Gln	Leu	Ala	Cys	Val	Trp	Ala	Arg	Thr
				605					610					615
Lys	Glu	Ala	Thr	Ser	Cys	His	Arg	Ala	Leu	Gly	Asp	Arg	Pro	Gly
				620					625					630
Leu	Ile	Ala	Ile	Leu	Ala	Leu	Ala	Val	Leu	Leu	Leu	Ala	Ala	Gly
				635					640					645
Leu	Ala	Ala	His	Leu	Gly	Thr	Gly	Gln	Pro	Arg	Lys	Gly	Val	Gly
				650					655					660
Gly	Arg	Arg	Pro	Leu	Pro	Pro	Ala	Trp	Ala	Phe	Trp	Gly	Trp	Ser
				665					670					675
Ala	Pro	Ser	Val	Arg	Val	Val	Ser	Ala	Pro	Leu	Val	Leu	Pro	Trp
				680					685					690
Asn	Pro	Gly	Arg	Lys	Leu	Pro	Arg	Ser	Ser	Glu	Gly	Glu	Thr	Leu
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<220>  
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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<213> Homo Sapien

<400> 250

Met Arg Gln Thr Ile Ile Lys Val Ile Lys Phe Ile Leu Ile Ile

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

1	5	10	15
Cys Tyr Thr Val Tyr Tyr Val His Asn Ile Lys Phe Asp Val Asp	20	25	30
Cys Thr Val Asp Ile Glu Ser Leu Thr Gly Tyr Arg Thr Tyr Arg	35	40	45
Cys Ala His Pro Leu Ala Thr Leu Phe Lys Ile Leu Ala Ser Phe	50	55	60
Tyr Ile Ser Leu Val Ile Phe Tyr Gly Leu Ile Cys Met Tyr Thr	65	70	75
Leu Trp Trp Met Leu Arg Arg Ser Leu Lys Lys Tyr Ser Phe Glu	80	85	90
Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys	95	100	105
Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln Tyr Asp Pro	110	115	120
Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu	125	130	135
Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu Asp	140	145	150
Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu	155	160	165
Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp	170	175	180
Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val	185	190	195
Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu	200	205	210
Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala	215	220	225
Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp	230	235	240
Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu	245	250	255
Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr	260	265	270
Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu	275	280	285
Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp	290	295	300
Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr	305	310	315

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr  
320 325 330

Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser  
335 340 345

Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn  
350 355 360

Asn Leu Lys Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu His  
365 370 375

Arg Leu Thr Cys Leu Lys Leu Trp Tyr Asn His Ile Ala Tyr Ile  
380 385 390

Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu  
395 400 405

Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys  
410 415 420

Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe  
425 430 435

Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala  
440 445 450

Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln  
455 460 465

Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln  
470 475 480

Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile  
485 490 495

Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly  
500 505 510

Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp  
515 520 525

Leu Phe Asn Thr Leu Pro Pro Glu Val Lys Glu Arg Leu Trp Arg  
530 535 540

Ala Asp Lys Glu Gln Ala  
545

<210> 251

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 251

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<210> 252

<211> 24

<212> DNA

<213> Artificial Sequence



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>

<223> Synthetic Oligonucleotide Probe

<400> 252

gatggctagg ttctggaggt tctg 24

<210> 253

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 253

caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<210> 254

<211> 1650

<212> DNA

<213> Homo Sapien

<400> 254

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 gcgctctccc gtcccgcggt ggttgctgct gctgccgctg ctgctgggcc 100  
 tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150  
 tgggattatg tgacgggtccg caaggatgcc tacatgttct ggtggctcta 200  
 ttatgccacc aactcctgca agaacttctc agaactgccc ctggatcatgt 250  
 ggcttcaggg cgggtccaggc ggttctagca ctggatttgg aaactttgag 300  
 gaaattgggc cccttgacag tgatctcaaa ccacggaaaa ccacctggct 350  
 ccaggctgcc agtctcctat ttgtggataa tcccgtgggc actgggttca 400  
 gttatgtgaa tggtagtggt gcctatgcca aggacctggc tatggtggct 450  
 tcagacatga tggttctcct gaagaccttc ttcagttgcc acaaagaatt 500  
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 aagtgcaact ttgcgggggt tgccttgagg gattcctgga tctcccctgt 650  
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 agaaatgatc attgaacaga acacagatgg ggtgaacttc tataacatct 850  
 taactaaaag cactcccacg tctacaatgg agtcgagtct agaattcaca 900  
 cagagccacc tagtttgtct ttgtcagcgc cacgtgagac acctacaacg 950  
 agatgcctta agccagctca tgaatggccc catcagaaag aagctcaaaa 1000

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 aacatggagg aggacttcat gaagccagtc attagcattg tggacgagtt 1100  
 gctggaggca gggatcaacg tgacggtgta taatggacag ctggatctca 1150  
 tcgtagatac catgggtcag gaggcctggg tgcggaaact gaagtggcca 1200  
 gaactgccta aattcagtc gctgaagtgg aaggccctgt acagtgaccc 1250  
 taaatctttg gaaacatctg cttttgtcaa gtcctacaag aaccttgctt 1300  
 tctactggat tctgaaagct ggtcatatgg ttccttctga ccaaggggac 1350  
 atggctctga agatgatgag actggtgact cagcaagaat aggatggatg 1400  
 gggctggaga tgagctggtt tggccttggg gcacagagct gagctgaggc 1450  
 cgctgaagct gtaggaagcg ccattcttcc ctgtatctaa ctggggctgt 1500  
 gatcaagaag gttctgacca gcttctgcag aggataaaat cattgtctct 1550  
 ggaggcaatt tggaatttat ttctgcttct taaaaaaacc taagattttt 1600  
 taaaaaattg atttgttttg atcaaaataa aggatgataa tagatattaa 1650

<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

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1				5					10					15
Leu	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp
			20						25					30
Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
			35						40					45
Arg	Lys	Asp	Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn
			50						55					60
Ser	Cys	Lys	Asn	Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln
			65						70					75
Gly	Gly	Pro	Gly	Gly	Ser	Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu
			80						85					90
Ile	Gly	Pro	Leu	Asp	Ser	Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp
			95						100					105
Leu	Gln	Ala	Ala	Ser	Leu	Leu	Phe	Val	Asp	Asn	Pro	Val	Gly	Thr
			110						115					120
Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	Gly	Ala	Tyr	Ala	Lys	Asp	Leu
			125						130					135
Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu	Leu	Lys	Thr	Phe	Phe
			140						145					150

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser  
 155 160 165  
 Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu  
 170 175 180  
 Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly  
 185 190 195  
 Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu  
 200 205 210  
 Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys  
 215 220 225  
 Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala  
 230 235 240  
 Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys  
 245 250 255  
 Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr  
 260 265 270  
 Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser  
 275 280 285  
 Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His  
 290 295 300  
 Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly  
 305 310 315  
 Pro Ile Arg Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp  
 320 325 330  
 Gly Gly Gln Ala Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe  
 335 340 345  
 Met Lys Pro Val Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly  
 350 355 360  
 Ile Asn Val Thr Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp  
 365 370 375  
 Thr Met Gly Gln Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu  
 380 385 390  
 Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp  
 395 400 405  
 Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn  
 410 415 420  
 Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro Ser  
 425 430 435  
 Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr Gln  
 440 445 450

Gln Glu

&lt;210&gt; 256

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150
tggagaggac gccgaactcg ggcgttgggc gtggcagggg agcctgcgcc 200
tgtgggattc ccacgtatgc ggagtgaacc tgctcagcca ccgctgggca 250
ctcacggcgg cgcactgctt tgaaacctat agtgacctta gtgatccctc 300
cgggtggatg gtccagtttg gccagctgac ttccatgcca tccttctgga 350
gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400
cctcgctacc tggggaattc accctatgac attgccttgg tgaagctgtc 450
tgcacctgtc acctacacta aacacatcca gcccatctgt ctccaggcct 500
ccacatttga gtttgagaac cggacagact gctgggtgac tggctggggg 550
tacatcaaag aggatgaggc actgccatct cccacacccc tccaggaagt 600
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<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

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 1           5           10          15
Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser
                20           25           30
Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Glu	Asp	Ala	Glu	Leu	Gly	Arg	Trp	Pro	Trp	Gln	Gly	Ser	Leu	Arg	35	40	45
				50					55					60			
Leu	Trp	Asp	Ser	His	Val	Cys	Gly	Val	Ser	Leu	Leu	Ser	His	Arg	65	70	75
				65										75			
Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu	80	85	90
				80										90			
Ser	Asp	Pro	Ser	Gly	Trp	Met	Val	Gln	Phe	Gly	Gln	Leu	Thr	Ser	95	100	105
				95										105			
Met	Pro	Ser	Phe	Trp	Ser	Leu	Gln	Ala	Tyr	Tyr	Thr	Arg	Tyr	Phe	110	115	120
				110										120			
Val	Ser	Asn	Ile	Tyr	Leu	Ser	Pro	Arg	Tyr	Leu	Gly	Asn	Ser	Pro	125	130	135
				125										135			
Tyr	Asp	Ile	Ala	Leu	Val	Lys	Leu	Ser	Ala	Pro	Val	Thr	Tyr	Thr	140	145	150
				140										150			
Lys	His	Ile	Gln	Pro	Ile	Cys	Leu	Gln	Ala	Ser	Thr	Phe	Glu	Phe	155	160	165
				155										165			
Glu	Asn	Arg	Thr	Asp	Cys	Trp	Val	Thr	Gly	Trp	Gly	Tyr	Ile	Lys	170	175	180
				170										180			
Glu	Asp	Glu	Ala	Leu	Pro	Ser	Pro	His	Thr	Leu	Gln	Glu	Val	Gln	185	190	195
				185										195			
Val	Ala	Ile	Ile	Asn	Asn	Ser	Met	Cys	Asn	His	Leu	Phe	Leu	Lys	200	205	210
				200										210			
Tyr	Ser	Phe	Arg	Lys	Asp	Ile	Phe	Gly	Asp	Met	Val	Cys	Ala	Gly	215	220	225
				215										225			
Asn	Ala	Gln	Gly	Gly	Lys	Asp	Ala	Cys	Phe	Gly	Asp	Ser	Gly	Gly	230	235	240
				230										240			
Pro	Leu	Ala	Cys	Asn	Lys	Asn	Gly	Leu	Trp	Tyr	Gln	Ile	Gly	Val	245	250	255
				245										255			
Val	Ser	Trp	Gly	Val	Gly	Cys	Gly	Arg	Pro	Asn	Arg	Pro	Gly	Val	260	265	270
				260										270			
Tyr	Thr	Asn	Ile	Ser	His	His	Phe	Glu	Trp	Ile	Gln	Lys	Leu	Met	275	280	285
				275										285			
Ala	Gln	Ser	Gly	Met	Ser	Gln	Pro	Asp	Pro	Ser	Trp	Pro	Leu	Leu	290	295	300
				290										300			
Phe	Phe	Pro	Leu	Leu	Trp	Ala	Leu	Pro	Leu	Leu	Gly	Pro	Val		305	310	
				305													

<210> 258  
 <211> 2427  
 <212> DNA  
 <213> Homo Sapien

<400> 258  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 cggagcccga ccagcggagg acgctgcccc caggctgggt gtccctgggc 150  
 cgtgcggacc ctgaggaaga gctgagtctc acctttgccc tgagacagca 200  
 gaatgtggaa agactctcgg agctggtgca ggctgtgtcg gatcccagct 250  
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 ggcacatcct tccaggaacc tttcctcatc acaaataaaa ttgttgacta 1250  
 tatcagtgggt ggtggcttca gcaatgtgtt cccacggcct tcataccagg 1300  
 aggaagctgt aacgaagtgc ctgagctcta gccccacct gccaccatcc 1350  
 agttacttca atgccagtgg ccgtgcctac ccagatgtgg ctgcactttc 1400  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
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 gtcccctgcc ctgaagctgg cagttcagtc ccttattctg ccctgttgga 1800  
 agccctgctg aaccctcaac tattgactgc tgcagacagc ttatctccct 1850  
 aaccctgaaa tgctgtgagc ttgacttgac tcccaaccct accatgctcc 1900  
 atcatactca ggtctcccta ctctgcctt agattcctca ataagatgct 1950  
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 ttactcttt cctaccctga catccagaaa caatggcctc cagtgcatac 2150  
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 ctgacatcta caaccattac catctcacta aataagactt tctatccaat 2400  
 aatgattgat acctcaaag taaaaaa 2427

<210> 259  
 <211> 556  
 <212> PRT  
 <213> Homo Sapien

<400> 259  
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 Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu  
 35 40 45  
 Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg  
 50 55 60  
 Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln  
 65 70 75  
 Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg  
 80 85 90  
 Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala  
 95 100 105  
 Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu  
 110 115 120

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Thr Cys Trp Leu	Ser 125	Ile Arg Gln Ala	Glu 130	Leu Leu Leu Pro	Gly 135
Ala Glu Phe His	His 140	Tyr Val Gly Gly	Pro 145	Thr Glu Thr His	Val 150
Val Arg Ser Pro	His 155	Pro Tyr Gln Leu	Pro 160	Gln Ala Leu Ala	Pro 165
His Val Asp Phe	Val 170	Gly Gly Leu His	Arg 175	Phe Pro Pro Thr	Ser 180
Ser Leu Arg Gln	Arg 185	Pro Glu Pro Gln	Val 190	Thr Gly Thr Val	Gly 195
Leu His Leu Gly	Val 200	Thr Pro Ser Val	Ile 205	Arg Lys Arg Tyr	Asn 210
Leu Thr Ser Gln	Asp 215	Val Gly Ser Gly	Thr 220	Ser Asn Asn Ser	Gln 225
Ala Cys Ala Gln	Phe 230	Leu Glu Gln Tyr	Phe 235	His Asp Ser Asp	Leu 240
Ala Gln Phe Met	Arg 245	Leu Phe Gly Gly	Asn 250	Phe Ala His Gln	Ala 255
Ser Val Ala Arg	Val 260	Val Gly Gln Gln	Gly 265	Arg Gly Arg Ala	Gly 270
Ile Glu Ala Ser	Leu 275	Asp Val Gln Tyr	Leu 280	Met Ser Ala Gly	Ala 285
Asn Ile Ser Thr	Trp 290	Val Tyr Ser Ser	Pro 295	Gly Arg His Glu	Gly 300
Gln Glu Pro Phe	Leu 305	Gln Trp Leu Met	Leu 310	Leu Ser Asn Glu	Ser 315
Ala Leu Pro His	Val 320	His Thr Val Ser	Tyr 325	Gly Asp Asp Glu	Asp 330
Ser Leu Ser Ser	Ala 335	Tyr Ile Gln Arg	Val 340	Asn Thr Glu Leu	Met 345
Lys Ala Ala Ala	Arg 350	Gly Leu Thr Leu	Leu 355	Phe Ala Ser Gly	Asp 360
Ser Gly Ala Gly	Cys 365	Trp Ser Val Ser	Gly 370	Arg His Gln Phe	Arg 375
Pro Thr Phe Pro	Ala 380	Ser Ser Pro Tyr	Val 385	Thr Thr Val Gly	Gly 390
Thr Ser Phe Gln	Glu 395	Pro Phe Leu Ile	Thr 400	Asn Glu Ile Val	Asp 405
Tyr Ile Ser Gly	Gly 410	Gly Phe Ser Asn	Val 415	Phe Pro Arg Pro	Ser 420
Tyr Gln Glu Glu	Ala 425	Val Thr Lys Phe	Leu 430	Ser Ser Ser Pro	His 435



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu	Pro	Pro	Ser	Ser	Tyr	Phe	Asn	Ala	Ser	Gly	Arg	Ala	Tyr	Pro
				440					445					450
Asp	Val	Ala	Ala	Leu	Ser	Asp	Gly	Tyr	Trp	Val	Val	Ser	Asn	Arg
				455					460					465
Val	Pro	Ile	Pro	Trp	Val	Ser	Gly	Thr	Ser	Ala	Ser	Thr	Pro	Val
				470					475					480
Phe	Gly	Gly	Ile	Leu	Ser	Leu	Ile	Asn	Glu	His	Arg	Ile	Leu	Ser
				485					490					495
Gly	Arg	Pro	Pro	Leu	Gly	Phe	Leu	Asn	Pro	Arg	Leu	Tyr	Gln	Gln
				500					505					510
His	Gly	Ala	Gly	Leu	Phe	Asp	Val	Thr	Arg	Gly	Cys	His	Glu	Ser
				515					520					525
Cys	Leu	Asp	Glu	Glu	Val	Glu	Gly	Gln	Gly	Phe	Cys	Ser	Gly	Pro
				530					535					540
Gly	Trp	Asp	Pro	Val	Thr	Gly	Trp	Gly	Thr	Pro	Thr	Ser	Gln	Leu
				545					550					555

Cys

<210> 260  
 <211> 1638  
 <212> DNA  
 <213> Homo Sapien

<400> 260  
 gccgcgcgct ctctcccggc gccacacact gtctgagcgg cgcagcgagc 50  
 cgcgccccgg gcgggctgct cggcgcgga cagtgtctcg catggcaggg 100  
 attccagggc tcctcttctt tctcttcttt ctgctctgtg ctgttgggca 150  
 agtgagccct tacagtgcc cctggaaacc cacttggcct gcataccgcc 200  
 tccctgtcgt cttgccccag tctaccctca atttagccaa gccagacttt 250  
 ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300  
 taagggaact cactgcccc cttacgaaga ggccaagcaa tatctgtctt 350  
 atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcatc 400  
 tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450  
 ttcaggaaag tctcgaagga agcggcagat ttatggctat gacagcaggt 500  
 tcagcatttt tgggaaggac ttcctgtctca actacccttt ctcaacatca 550  
 gtgaagttat ccacgggctg caccggcacc ctggtggcag agaagcatgt 600  
 cctcacagct gccactgca tacacgatgg aaaaacctat gtgaaaggaa 650  
 cccagaagct tcgagtgggc ttcctaaagc ccaagtttaa agatgggtgt 700  
 cgaggggcca acgactccac ttcagccatg cccgagcaga tgaaatttca 750

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

gtggatccgg gtgaaacgca cccatgtgcc caaggggttg atcaaggga 800  
atgccaatga catcggcatg gattatgatt atgccctcct ggaactcaaa 850  
aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctcttgctaa 900  
gcagctgcca gggggcagaa ttcacttctc tggttatgac aatgaccgac 950  
caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000  
ttgctctacc agcaatgcga tgcccagcca ggggccagcg ggtctggggt 1050  
ctatgtgagg atgtggaaga gacagcagca gaagtgggag cgaaaaatta 1100  
ttggcatttt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150  
gatttcaacg tggctgtcag aatcactcct ctcaaataatg cccagatttg 1200  
ctattggatt aaaggaaact acctggattg tagggagggg tgacacagtg 1250  
ttccctcctg gcagcaatta agggctcttca tgttcttatt ttaggagagg 1300  
ccaaattggt ttttgtcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgtg 1350  
tgtgtgtaag gtgtcttata atcttttacc tatttcttac aattgcaaga 1400  
tgactggctt tactatttga aaactggttt gtgtatcata tcatatatca 1450  
tttaagcagt ttgaaggcat acttttgcac agaaataaaa aaaatactga 1500  
tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgtttttg 1550  
caaactttga tttttatttc atctgaactt gtttcaaaga tttatattaa 1600  
atatttgga tacaagagat atgaaaaaaaa aaaaaaaaa 1638

<210> 261  
<211> 383  
<212> PRT  
<213> Homo Sapien

<400> 261  
Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu  
1 5 10 15  
Cys Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro  
20 25 30  
Thr Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr  
35 40 45  
Leu Asn Leu Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu  
50 55 60  
Val Ser Ser Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu  
65 70 75  
Pro Thr Tyr Glu Glu Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu  
80 85 90  
Tyr Ala Asn Gly Ser Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile  
95 100 105

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Ser Ser Ser	Gly 110	Asp Gly Ala Gln	His 115	Arg Asp Ser Gly	Ser 120
Ser Gly Lys Ser	Arg 125	Arg Lys Arg Gln	Ile 130	Tyr Gly Tyr Asp	Ser 135
Arg Phe Ser Ile	Phe 140	Gly Lys Asp Phe	Leu 145	Leu Asn Tyr Pro	Phe 150
Ser Thr Ser Val	Lys 155	Leu Ser Thr Gly	Cys 160	Thr Gly Thr Leu	Val 165
Ala Glu Lys His	Val 170	Leu Thr Ala Ala	His 175	Cys Ile His Asp	Gly 180
Lys Thr Tyr Val	Lys 185	Gly Thr Gln Lys	Leu 190	Arg Val Gly Phe	Leu 195
Lys Pro Lys Phe	Lys 200	Asp Gly Gly Arg	Gly 205	Ala Asn Asp Ser	Thr 210
Ser Ala Met Pro	Glu 215	Gln Met Lys Phe	Gln 220	Trp Ile Arg Val	Lys 225
Arg Thr His Val	Pro 230	Lys Gly Trp Ile	Lys 235	Gly Asn Ala Asn	Asp 240
Ile Gly Met Asp	Tyr 245	Asp Tyr Ala Leu	Leu 250	Glu Leu Lys Lys	Pro 255
His Lys Arg Lys	Phe 260	Met Lys Ile Gly	Val 265	Ser Pro Pro Ala	Lys 270
Gln Leu Pro Gly	Gly 275	Arg Ile His Phe	Ser 280	Gly Tyr Asp Asn	Asp 285
Arg Pro Gly Asn	Leu 290	Val Tyr Arg Phe	Cys 295	Asp Val Lys Asp	Glu 300
Thr Tyr Asp Leu	Leu 305	Tyr Gln Gln Cys	Asp 310	Ala Gln Pro Gly	Ala 315
Ser Gly Ser Gly	Val 320	Tyr Val Arg Met	Trp 325	Lys Arg Gln Gln	Gln 330
Lys Trp Glu Arg	Lys 335	Ile Ile Gly Ile	Phe 340	Ser Gly His Gln	Trp 345
Val Asp Met Asn	Gly 350	Ser Pro Gln Asp	Phe 355	Asn Val Ala Val	Arg 360
Ile Thr Pro Leu	Lys 365	Tyr Ala Gln Ile	Cys 370	Tyr Trp Ile Lys	Gly 375
Asn Tyr Leu Asp	Cys 380	Arg Glu Gly			

<210> 262  
 <211> 1378  
 <212> DNA  
 <213> Homo Sapien

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 262

gcatcgccct gggctctctcg agcctgctgc ctgctcccc gccccaccag 50  
ccatggtggt ttctggagcg cccccagccc tgggtggggg ctgtctcggc 100  
accttcacct ccctgctgct gctggcgtcg acagccatcc tcaatgcggc 150  
caggatacct gttccccag cctgtgggaa gccccagcag ctgaaccggg 200  
ttgtgggcgg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250  
atccagaaga atgggaccca ccactgcgca ggttctctgc tcaccagccg 300  
ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaaccat 350  
acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400  
cggctccaga aggtgggtgt tgcctgggtg gagccccacc ctgtgtattc 450  
ctggaaggaa ggtgcctgtg cagacattgc cctggtgcgt ctcgagcgct 500  
ccatacagtt ctgagagcgg gtcctgcca tctgcctacc tgatgcctct 550  
atccacctcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600  
ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650  
ttcctatcat cgactcggaa gtctgcagcc atctgtactg gcggggagca 700  
ggacagggac ccatcactga ggacatgctg tgtgccggct acttgagggg 750  
ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800  
tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggtgt 850  
gccgagcgca acaggccccg ggtctacatc agcctctctg cgcaccgctc 900  
ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg 950  
ggggtggggc cctcagggca ccgagccagg gctctggggc cgccgcgcgc 1000  
tcctagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050  
cacatctgga tctggatctg cggcggcctc gggcggtttc ccccgccgta 1100  
aataggctca tctacctcta cctctggggg cccggacggc tgctgcggaa 1150  
aggaaacccc ctccccgacc cgcccagcgg cctcaggccc ccctccaagg 1200  
catcaggccc cgccaacgg cctcatgtcc ccgccccac gacttccggc 1250  
cccgcccccg ggccccagcg cttttgtgta tataaatgtt aatgattttt 1300  
ataggatttt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350  
ataaattatt tattctccaa aaaaaaaa 1378

<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu	1	5	10	15
Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu	20	25	30	
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln	35	40	45	
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu	50	55	60	
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys	65	70	75	
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	80	85	90	
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu	95	100	105	
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys	110	115	120	
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys	125	130	135	
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser	140	145	150	
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala	155	160	165	
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp	170	175	180	
Gly	Ser	Ile	Gln	Asp	Gly	Val	Pro	Leu	Pro	His	Pro	Gln	Thr	Leu	185	190	195	
Gln	Lys	Leu	Lys	Val	Pro	Ile	Ile	Asp	Ser	Glu	Val	Cys	Ser	His	200	205	210	
Leu	Tyr	Trp	Arg	Gly	Ala	Gly	Gln	Gly	Pro	Ile	Thr	Glu	Asp	Met	215	220	225	
Leu	Cys	Ala	Gly	Tyr	Leu	Glu	Gly	Glu	Arg	Asp	Ala	Cys	Leu	Gly	230	235	240	
Asp	Ser	Gly	Gly	Pro	Leu	Met	Cys	Gln	Val	Asp	Gly	Ala	Trp	Leu	245	250	255	
Leu	Ala	Gly	Ile	Ile	Ser	Trp	Gly	Glu	Gly	Cys	Ala	Glu	Arg	Asn	260	265	270	
Arg	Pro	Gly	Val	Tyr	Ile	Ser	Leu	Ser	Ala	His	Arg	Ser	Trp	Val	275	280	285	
Glu	Lys	Ile	Val	Gln	Gly	Val	Gln	Leu	Arg	Gly	Arg	Ala	Gln	Gly	290	295	300	
Gly	Gly	Ala	Leu	Arg	Ala	Pro	Ser	Gln	Gly	Ser	Gly	Ala	Ala	Ala	305	310	315	

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

gtccgcaagg atgcctacat gttc 24

<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagaggtgt ctaaggttg 19

<210> 266

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 266

agctctagac caatgccagc ttcc 24

<210> 267

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 267

gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<210> 268

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 268

ggggaattca ccctatgaca ttgcc 25

<210> 269

<211> 24

<212> DNA

<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>

<223> Synthetic Oligonucleotide Probe

<400> 269

gaatgccctg caagcatcaa ctgg 24

<210> 270

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 270

gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 271

gcggaagggc agaatgggac tccaag 26

<210> 272

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 272

cagccctgcc acatgtgc 18

<210> 273

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 273

tactgggtgg tcagcaac 18

<210> 274

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 274

ggcgaagagc agggtgagac cccg 24

<210> 275

<211> 45

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 275  
gccctcatcc tctctggcaa atgcagttac agcccggagc ccgac 45

<210> 276  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 276  
gggcagggat tccagggctc c 21

<210> 277  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 277  
ggctatgaca gcaggttc 18

<210> 278  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 278  
tgacaatgac cgaccagg 18

<210> 279  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 279  
gcatcgcatt gctggtagag caag 24

<210> 280  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 280



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
ttacagtgcc ccctggaaac ccacttggcc tgcataccgc ctccc 45

<210> 281  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 281  
cgtctcgagc gtcctatata gttcccttgc ccca 34

<210> 282  
<211> 61  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 282  
tggaggggga gcgggatgct tgtctgggag actccggggg cccctcatg 50  
tgccaggtgg a 61

<210> 283  
<211> 119  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 283  
ccctcagacc ctgcagaagc tgaagggtcc tatcatcgac tcggaagtct 50  
gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100  
atgctgtgtg ccggctact 119

<210> 284  
<211> 1875  
<212> DNA  
<213> Homo Sapien

<400> 284  
gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50  
ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100  
agatgaggag aaacgtttga tggaggagct gcacaacctc taccggggccc 150  
aggatatccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200  
ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250  
caaggagcgc gggcgccgag gcgagaatct gttcgccatc acagacgagg 300  
gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350  
tacaacctca gcgcccgcac ctgcagccca ggccagatgt gcggccacta 400

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

cacgcaggtg gtatgggcca agacagagag gatcggctgt gggtcccact 450  
tctgtgagaa gctccagggg gttgaggaga ccaacatcga attactggtg 500  
tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550  
ggggactccg tgctcccaat gtccctctgg ctaccactgc aagaactccc 600  
tctgtgaacc catcggaagc ccggaagatg ctcaggattt gccttacctg 650  
gtaactgagg ccccatcctt ccgggcgact gaagcatcag actctaggaa 700  
aatgggtact ctttcttccc tagcaacggg gattccggct ttcttggtaa 750  
cagaggtctc aggctcccgt gcaaccaagg ctctgcctgc tgtggaaacc 800  
caggcccca cttccttagc aacgaaagac ccgccctcca tggcaacaga 850  
ggctccacct tgcgtaacaa ctgagggtccc ttccattttg gcagctcaca 900  
gcctgcctc cttggatgag gagccagtta cttccccaa atcgacccat 950  
gttcctatcc caaaatcagc agacaaagt acagacaaaa caaaagtgcc 1000  
ctctaggagc ccagagaact ctctggacct caagatgtcc ctgacagggg 1050  
caagggaact cctaccccat gccaggagg aggctgaggc tgaggctgag 1100  
ttgcctcctt ccagtgaggt cttggcctca gtttttccag cccaggacaa 1150  
gccagggtgag ctgcaggcca cactggacca cacggggcac acctcctcca 1200  
agtccctgcc caatttcccc aatacctctg ccaccgctaa tgccacgggt 1250  
gggcgtgccc tggctctgca gtcgtccttg ccagggtgcag agggccctga 1300  
caagcctagc gttgtgtcag ggctgaactc gggccctggg catgtgtggg 1350  
gccctctcct gggactactg ctctgcctc ctctgggtgt ggctggaatc 1400  
ttctgaatgg gataccactc aaagggtgaa gaggtcagct gtcctcctgt 1450  
catcttcccc accctgtccc cagcccctaa acaagatact tcttggttaa 1500  
ggccctccgg aagggaaagg ctacggggca tgtgcctcat cacaccatcc 1550  
atcctggagg cacaaggcct ggctggctgc gagctcagga ggccgcctga 1600  
ggactgcaca ccgggcccac acctctcctg cccctccctc ctgagtcctg 1650  
gggggtgggag gatttgaggg agctcactgc ctacctggcc tggggctgtc 1700  
tgccacaca gcatgtgcgc tctccctgag tgctgtgta gctggggatg 1750  
gggattccta ggggcagatg aaggacaagc cccactggag tggggttctt 1800  
tgagtggggg aggcagggac gagggaagga aagtaactcc tgactctcca 1850  
ataaaaacct gtccaacctg tgaaa 1875

<210> 285  
<211> 463  
<212> PRT

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<213> Homo Sapien

<400> 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu	1	5	10	15
Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp	20	25	30	
Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala	35	40	45	
Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp	50	55	60	
Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val	65	70	75	
Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe	80	85	90	
Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu	95	100	105	
Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys	110	115	120	
Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	125	130	135	
Lys	Thr	Glu	Arg	Ile	Gly	Cys	Gly	Ser	His	Phe	Cys	Glu	Lys	Leu	140	145	150	
Gln	Gly	Val	Glu	Glu	Thr	Asn	Ile	Glu	Leu	Leu	Val	Cys	Asn	Tyr	155	160	165	
Glu	Pro	Pro	Gly	Asn	Val	Lys	Gly	Lys	Arg	Pro	Tyr	Gln	Glu	Gly	170	175	180	
Thr	Pro	Cys	Ser	Gln	Cys	Pro	Ser	Gly	Tyr	His	Cys	Lys	Asn	Ser	185	190	195	
Leu	Cys	Glu	Pro	Ile	Gly	Ser	Pro	Glu	Asp	Ala	Gln	Asp	Leu	Pro	200	205	210	
Tyr	Leu	Val	Thr	Glu	Ala	Pro	Ser	Phe	Arg	Ala	Thr	Glu	Ala	Ser	215	220	225	
Asp	Ser	Arg	Lys	Met	Gly	Thr	Pro	Ser	Ser	Leu	Ala	Thr	Gly	Ile	230	235	240	
Pro	Ala	Phe	Leu	Val	Thr	Glu	Val	Ser	Gly	Ser	Leu	Ala	Thr	Lys	245	250	255	
Ala	Leu	Pro	Ala	Val	Glu	Thr	Gln	Ala	Pro	Thr	Ser	Leu	Ala	Thr	260	265	270	
Lys	Asp	Pro	Pro	Ser	Met	Ala	Thr	Glu	Ala	Pro	Pro	Cys	Val	Thr	275	280	285	
Thr	Glu	Val	Pro	Ser	Ile	Leu	Ala	Ala	His	Ser	Leu	Pro	Ser	Leu	290	295	300	

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile	305	310	315
Pro Lys Ser Ala Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser	320	325	330
Arg Ser Pro Glu Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly	335	340	345
Ala Arg Glu Leu Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu	350	355	360
Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro	365	370	375
Ala Gln Asp Lys Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr	380	385	390
Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser	395	400	405
Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser	410	415	420
Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser	425	430	435
Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly	440	445	450
Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe	455	460	

<210> 286

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

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<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<213> Homo Sapien

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

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				20					25					30
Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu
				35					40					45
Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser
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Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu
				65					70					75
Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu
				80					85					90
Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro
				95					100					105
Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr
				110					115					120
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu
				125					130					135

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys	140	145	150
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn	155	160	165
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala	170	175	180
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met	185	190	195
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu	200	205	210
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly	215	220	225
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn	230	235	240
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu	245	250	255
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser	260	265	270
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn	275	280	285
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser	290	295	300
Leu	Lys	Thr	Leu	Asp	Leu	Lys	Asn	Asn	Glu	Ile	Ser	Trp	Thr	Ile	305	310	315
Glu	Asp	Met	Asn	Gly	Ala	Phe	Ser	Gly	Leu	Asp	Lys	Leu	Arg	Arg	320	325	330
Leu	Ile	Leu	Gln	Gly	Asn	Arg	Ile	Arg	Ser	Ile	Thr	Lys	Lys	Ala	335	340	345
Phe	Thr	Gly	Leu	Asp	Ala	Leu	Glu	His	Leu	Asp	Leu	Ser	Asp	Asn	350	355	360
Ala	Ile	Met	Ser	Leu	Gln	Gly	Asn	Ala	Phe	Ser	Gln	Met	Lys	Lys	365	370	375
Leu	Gln	Gln	Leu	His	Leu	Asn	Thr	Ser	Ser	Leu	Leu	Cys	Asp	Cys	380	385	390
Gln	Leu	Lys	Trp	Leu	Pro	Gln	Trp	Val	Ala	Glu	Asn	Asn	Phe	Gln	395	400	405
Ser	Phe	Val	Asn	Ala	Ser	Cys	Ala	His	Pro	Gln	Leu	Leu	Lys	Gly	410	415	420
Arg	Ser	Ile	Phe	Ala	Val	Ser	Pro	Asp	Gly	Phe	Val	Cys	Asp	Asp	425	430	435
Phe	Pro	Lys	Pro	Gln	Ile	Thr	Val	Gln	Pro	Glu	Thr	Gln	Ser	Ala			



## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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Ser Asp Ser Pro Met	Thr Phe Ala Trp	Lys Lys Asp Asn	Glu Leu		
	455		460		465
	470		475		480
Leu His Asp Ala	Glu Met Glu Asn Tyr	Ala His Leu Arg Ala	Gln		
	485		490		495
Gly Gly Glu Val	Met Glu Tyr Thr Thr	Ile Leu Arg Leu Arg	Glu		
	500		505		510
Val Glu Phe Ala	Ser Glu Gly Lys Tyr	Gln Cys Val Ile Ser	Asn		
	515		520		525
His Phe Gly Ser	Ser Tyr Ser Val Lys	Ala Lys Leu Thr Val	Asn		
	530		535		540
Met Leu Pro Ser	Phe Thr Lys Thr Pro	Met Asp Leu Thr Ile	Arg		
	545		550		555
Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His	Pro		
	560		565		570
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe	Pro		
	575		580		585
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp	Val		
	590		595		600
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr	Ser		
	605		610		615
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala	Thr		
	620		625		630
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu	Asp		
	635		640		645
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile	Ala		
	650		655		660
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp	Ser		
	665		670		675
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn	Gln		
	680		685		690
Leu Leu Ile Ile	Val Asp Ser Asp Val	Ser Asp Ala Gly Lys	Tyr		
	695		700		705
Thr Cys Glu Met	Ser Asn Thr Leu Gly	Thr Glu Arg Gly Asn	Val		
	710		715		720
Arg Leu Ser Val	Ile Pro Thr Pro Thr	Cys Asp Ser Pro Gln	Met		
	725		730		735
Thr Ala Pro Ser	Leu Asp Asp Asp Gly	Trp Ala Thr Val Gly	Val		
	740		745		750

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val  
755 760 765

Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys  
770 775 780

Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro  
785 790 795

Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly  
800 805 810

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser  
815 820 825

Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
830 835 840

Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
845 850 855

Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr  
860 865 870

Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His  
875 880 885

Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr  
890 895 900

Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His  
905 910 915

Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp  
920 925 930

Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
935 940 945

Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu  
950 955 960

Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn  
965 970 975

Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu  
980 985 990

Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg  
995 1000 1005

Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly  
1010 1015 1020

Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn  
1025 1030 1035

His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro  
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Asn Phe Gln Ser Tyr Asp Leu Asp Thr  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 <213> Homo Sapien

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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;211&gt; 640

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 292

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Leu  Ala Leu Gln Leu Leu Val Val Ala  Gly Leu Val Arg Ala Gln
          35          40          45
Thr  Cys Pro Ser Val  Cys Ser Cys Ser  Asn Gln Phe Ser Lys Val
          50          55          60
Ile  Cys Val Arg Lys  Asn Leu Arg Glu Val  Pro Asp Gly Ile Ser
          65          70          75
Thr  Asn Thr Arg Leu Leu Asn Leu His  Glu Asn Gln Ile Gln Ile
          80          85          90
Ile  Lys Val Asn Ser  Phe Lys His Leu Arg His Leu Glu Ile Leu
          95          100          105
Gln  Leu Ser Arg Asn His Ile Arg Thr  Ile Glu Ile Gly Ala Phe
          110          115          120
Asn  Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg
          125          130          135
Leu  Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu
          140          145          150
Lys  Glu Leu Trp Leu Arg Asn Asn Pro  Ile Glu Ser Ile Pro Ser
          155          160          165
Tyr  Ala Phe Asn Arg  Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly
          170          175          180
Glu  Leu Lys Arg Leu Ser Tyr Ile Ser  Glu Gly Ala Phe Glu Gly
          185          190          195
Leu  Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg
          200          205          210
Glu  Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp
          215          220          225
Leu  Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln
          230          235          240
Gly  Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile
          245          250          255
Gln  Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val
          260          265          270
Glu  Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp
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Leu  Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Asn Pro Trp Asn	Cys 305	Asn Cys Asp Ile	Leu 310	Trp Leu Ser Trp	Trp 315
Ile Lys Asp Met	Ala 320	Pro Ser Asn Thr	Ala 325	Cys Cys Ala Arg	Cys 330
Asn Thr Pro Pro	Asn 335	Leu Lys Gly Arg	Tyr 340	Ile Gly Glu Leu	Asp 345
Gln Asn Tyr Phe	Thr 350	Cys Tyr Ala Pro	Val 355	Ile Val Glu Pro	Pro 360
Ala Asp Leu Asn	Val 365	Thr Glu Gly Met	Ala 370	Ala Glu Leu Lys	Cys 375
Arg Ala Ser Thr	Ser 380	Leu Thr Ser Val	Ser 385	Trp Ile Thr Pro	Asn 390
Gly Thr Val Met	Thr 395	His Gly Ala Tyr	Lys 400	Val Arg Ile Ala	Val 405
Leu Ser Asp Gly	Thr 410	Leu Asn Phe Thr	Asn 415	Val Thr Val Gln	Asp 420
Thr Gly Met Tyr	Thr 425	Cys Met Val Ser	Asn 430	Ser Val Gly Asn	Thr 435
Thr Ala Ser Ala	Thr 440	Leu Asn Val Thr	Ala 445	Ala Thr Thr Thr	Pro 450
Phe Ser Tyr Phe	Ser 455	Thr Val Thr Val	Glu 460	Thr Met Glu Pro	Ser 465
Gln Asp Glu Ala	Arg 470	Thr Thr Asp Asn	Asn 475	Val Gly Pro Thr	Pro 480
Val Val Asp Trp	Glu 485	Thr Thr Asn Val	Thr 490	Thr Ser Leu Thr	Pro 495
Gln Ser Thr Arg	Ser 500	Thr Glu Lys Thr	Phe 505	Thr Ile Pro Val	Thr 510
Asp Ile Asn Ser	Gly 515	Ile Pro Gly Ile	Asp 520	Glu Val Met Lys	Thr 525
Thr Lys Ile Ile	Ile 530	Gly Cys Phe Val	Ala 535	Ile Thr Leu Met	Ala 540
Ala Val Met Leu	Val 545	Ile Phe Tyr Lys	Met 550	Arg Lys Gln His	His 555
Arg Gln Asn His	His 560	Ala Pro Thr Arg	Thr 565	Val Glu Ile Ile	Asn 570
Val Asp Asp Glu	Ile 575	Thr Gly Asp Thr	Pro 580	Met Glu Ser His	Leu 585
Pro Met Pro Ala	Ile 590	Glu His Glu His	Leu 595	Asn His Tyr Asn	Ser 600
Tyr Lys Ser Pro	Phe Asn His Thr Thr	Thr Val Asn Thr Ile Asn			

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
605 610 615

Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn  
620 625 630

Ser Lys Asp Asn Val Gln Glu Thr Gln Ile  
635 640

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<211> 4053  
<212> DNA

<213> Homo Sapien

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aaagaaggaa ttgaccgggc agcgcgaggg aggagcgcgc acgcgaccgc 150  
gagggcgggc gtgcaccctc ggctggaagt ttgtgccggg ccccgagcgc 200  
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gcgcgccgag cctccgtgcg cgcgccgcgg gggtggggct gctgctgtgc 300  
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cgggcagccc tctggggtag ccgccgagcg cccatgcccc actacctgcc 400  
gctgcctcgg ggacctgctg gactgcagtc gtaagcggct agcgcgtctt 450  
cccgagccac tcccgtcctg ggtcgtcgg ctggacttaa gtcacaacag 500  
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gtctcggcaa atattacact tctctccttg gctggaaaca ggattgttga 650  
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ctcaaatatc tgtatctcaa cagcaaccga gtcacatcaa tggaacctgg 800  
gtattttgac aatttgcca acacactcct tgtgttaaag ctgaacagga 850  
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catctcgaat tgaaccgaaa caagattaaa aatgtagatg gactgacatt 950  
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cgaaacttat ggatggagct ttttgggggc tgagcaacat ggaaattttg 1050  
cagctggacc ataacaacct aacagagatt accaaaggct ggctttacgg 1100  
cttgctgatg ctgcaggaac ttcattctcag ccaaaatgcc atcaacagga 1150  
tcagccctga tgcctgggag ttctgccaga agctcagtga gctggaccta 1200

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

acttttcaatc acttatcaag gtttagatgat tcaagcttcc ttggcctaag 1250  
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attgtgcctt ccgggggctt tccagtttaa agactttgga tctgaagaac 1350  
aatgaaattt cctggactat tgaagacatg aatggtgctt tctctgggct 1400  
tgacaaactg aggcgactga tactccaagg aaatcggatc cgttctatta 1450  
ctaaaaaagc cttcactggt ttggatgcat tggagcatct agacctgagt 1500  
gacaacgcaa tcatgtcttt acaaggcaat gcattttcac aaatgaagaa 1550  
actgcaacaa ttgcatttaa atacatcaag ctttttgtgc gattgccagc 1600  
taaaatggct cccacagtgg gtggcgga aaactttca gagctttgta 1650  
aatgccagtt gtgcccattc tcagctgcta aaaggaagaa gcatttttgc 1700  
tgtagccca gatggctttg tgtgtgatga ttttcccaa cccagatca 1750  
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cactgttggga ccgaactgta accaagggag aaacagccgt cctacagtgc 2400  
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cccattggtg gtaaccgaga ggcacttttt tgcagcaggc aatcagcttc 2500  
tgattattgt ggactcagat gtcagtgatg ctgggaaata cacatgtgag 2550  
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gtggtgggca cgtcactcgt gtgggtggtc atcatatacc acacaaggcg 2750  
gaggaatgaa gattgcagca ttaccaacac agatgagacc aacttgccag 2800



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

cagatattcc tagttatttg tcatctcagg gaacgttagc tgacaggcag 2850  
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 ttcagggtgct ggatttttct taccacaaca tgacagtagt gggacctgcc 2950  
 atattgacaa tagcagtga gctgatgtgg aagctgccac agatctgttc 3000  
 ctttgtccgt ttttgggatc cacaggccct atgtatttga agggaaatgt 3050  
 gtatggctca gatccttttg aaacatatca tacaggttgc agtcctgacc 3100  
 caagaacagt tttaatggac cactatgagc ccagttacat aaagaaaaag 3150  
 gagtgtacc catgtttctca tccttcagaa gaatcctgcg aacggagctt 3200  
 cagtaatata tcgtggcctt cacatgtgag gaagctactt aacactagtt 3250  
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 tcttttagatt ttagtgcaaa tccagagcca gcgtcggttg cctcgagtaa 3350  
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 aaaaagttat gaaaattttt atactgggaa tgatgctcat ataagaatac 3800  
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 aaa 4053

<210> 294  
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 <212> PRT  
 <213> Homo Sapien

<400> 294  
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Leu Leu Cys Ala Val Leu Gly Arg Ala Gly Arg Ser Asp Ser Gly

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Gly	Arg	Gly	Glu	Leu	Gly	Gln	Pro	Ser	Gly	Val	Ala	Ala	Glu	Arg
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Pro	Cys	Pro	Thr	Thr	Cys	Arg	Cys	Leu	Gly	Asp	Leu	Leu	Asp	Cys
				50					55					60
Ser	Arg	Lys	Arg	Leu	Ala	Arg	Leu	Pro	Glu	Pro	Leu	Pro	Ser	Trp
				65					70					75
Val	Ala	Arg	Leu	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys
				80					85					90
Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu
				95					100					105
Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser
				110					115					120
Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu
				125					130					135
Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu
				140					145					150
Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro
				155					160					165
Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr
				170					175					180
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu
				185					190					195
Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys
				200					205					210
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn
				215					220					225
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala
				230					235					240
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met
				245					250					255
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu
				260					265					270
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly
				275					280					285
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn
				290					295					300
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu
				305					310					315
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser
				320					325					330
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Arg Val Ser Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser
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Leu Lys Thr Leu	Asp	Leu	Lys	Asn	Asn	Glu	Ile	Ser	Trp	Thr	Ile
	365					370					375
Glu Asp Met Asn	Gly	Ala	Phe	Ser	Gly	Leu	Asp	Lys	Leu	Arg	Arg
	380					385					390
Leu Ile Leu Gln	Gly	Asn	Arg	Ile	Arg	Ser	Ile	Thr	Lys	Lys	Ala
	395					400					405
Phe Thr Gly Leu	Asp	Ala	Leu	Glu	His	Leu	Asp	Leu	Ser	Asp	Asn
	410					415					420
Ala Ile Met Ser	Leu	Gln	Gly	Asn	Ala	Phe	Ser	Gln	Met	Lys	Lys
	425					430					435
Leu Gln Gln Leu	His	Leu	Asn	Thr	Ser	Ser	Leu	Leu	Cys	Asp	Cys
	440					445					450
Gln Leu Lys Trp	Leu	Pro	Gln	Trp	Val	Ala	Glu	Asn	Asn	Phe	Gln
	455					460					465
Ser Phe Val Asn	Ala	Ser	Cys	Ala	His	Pro	Gln	Leu	Leu	Lys	Gly
	470					475					480
Arg Ser Ile Phe	Ala	Val	Ser	Pro	Asp	Gly	Phe	Val	Cys	Asp	Asp
	485					490					495
Phe Pro Lys Pro	Gln	Ile	Thr	Val	Gln	Pro	Glu	Thr	Gln	Ser	Ala
	500					505					510
Ile Lys Gly Ser	Asn	Leu	Ser	Phe	Ile	Cys	Ser	Ala	Ala	Ser	Ser
	515					520					525
Ser Asp Ser Pro	Met	Thr	Phe	Ala	Trp	Lys	Lys	Asp	Asn	Glu	Leu
	530					535					540
Leu His Asp Ala	Glu	Met	Glu	Asn	Tyr	Ala	His	Leu	Arg	Ala	Gln
	545					550					555
Gly Gly Glu Val	Met	Glu	Tyr	Thr	Thr	Ile	Leu	Arg	Leu	Arg	Glu
	560					565					570
Val Glu Phe Ala	Ser	Glu	Gly	Lys	Tyr	Gln	Cys	Val	Ile	Ser	Asn
	575					580					585
His Phe Gly Ser	Ser	Tyr	Ser	Val	Lys	Ala	Lys	Leu	Thr	Val	Asn
	590					595					600
Met Leu Pro Ser	Phe	Thr	Lys	Thr	Pro	Met	Asp	Leu	Thr	Ile	Arg
	605					610					615
Ala Gly Ala Met	Ala	Arg	Leu	Glu	Cys	Ala	Ala	Val	Gly	His	Pro
	620					625					630
Ala Pro Gln Ile	Ala	Trp	Gln	Lys	Asp	Gly	Gly	Thr	Asp	Phe	Pro
	635					640					645
Ala Ala Arg Glu	Arg	Arg	Met	His	Val	Met	Pro	Glu	Asp	Asp	Val

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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				665					670					675
Cys	Thr	Ala	Gln	Asn	Ser	Ala	Gly	Ser	Ile	Ser	Ala	Asn	Ala	Thr
				680					685					690
Leu	Thr	Val	Leu	Glu	Thr	Pro	Ser	Phe	Leu	Arg	Pro	Leu	Leu	Asp
				695					700					705
Arg	Thr	Val	Thr	Lys	Gly	Glu	Thr	Ala	Val	Leu	Gln	Cys	Ile	Ala
				710					715					720
Gly	Gly	Ser	Pro	Pro	Pro	Lys	Leu	Asn	Trp	Thr	Lys	Asp	Asp	Ser
				725					730					735
Pro	Leu	Val	Val	Thr	Glu	Arg	His	Phe	Phe	Ala	Ala	Gly	Asn	Gln
				740					745					750
Leu	Leu	Ile	Ile	Val	Asp	Ser	Asp	Val	Ser	Asp	Ala	Gly	Lys	Tyr
				755					760					765
Thr	Cys	Glu	Met	Ser	Asn	Thr	Leu	Gly	Thr	Glu	Arg	Gly	Asn	Val
				770					775					780
Arg	Leu	Ser	Val	Ile	Pro	Thr	Pro	Thr	Cys	Asp	Ser	Pro	Gln	Met
				785					790					795
Thr	Ala	Pro	Ser	Leu	Asp	Asp	Asp	Gly	Trp	Ala	Thr	Val	Gly	Val
				800					805					810
Val	Ile	Ile	Ala	Val	Val	Cys	Cys	Val	Val	Gly	Thr	Ser	Leu	Val
				815					820					825
Trp	Val	Val	Ile	Ile	Tyr	His	Thr	Arg	Arg	Arg	Asn	Glu	Asp	Cys
				830					835					840
Ser	Ile	Thr	Asn	Thr	Asp	Glu	Thr	Asn	Leu	Pro	Ala	Asp	Ile	Pro
				845					850					855
Ser	Tyr	Leu	Ser	Ser	Gln	Gly	Thr	Leu	Ala	Asp	Arg	Gln	Asp	Gly
				860					865					870
Tyr	Val	Ser	Ser	Glu	Ser	Gly	Ser	His	His	Gln	Phe	Val	Thr	Ser
				875					880					885
Ser	Gly	Ala	Gly	Phe	Phe	Leu	Pro	Gln	His	Asp	Ser	Ser	Gly	Thr
				890					895					900
Cys	His	Ile	Asp	Asn	Ser	Ser	Glu	Ala	Asp	Val	Glu	Ala	Ala	Thr
				905					910					915
Asp	Leu	Phe	Leu	Cys	Pro	Phe	Leu	Gly	Ser	Thr	Gly	Pro	Met	Tyr
				920					925					930
Leu	Lys	Gly	Asn	Val	Tyr	Gly	Ser	Asp	Pro	Phe	Glu	Thr	Tyr	His
				935					940					945
Thr	Gly	Cys	Ser	Pro	Asp	Pro	Arg	Thr	Val	Leu	Met	Asp	His	Tyr
				950					955					960
Glu	Pro	Ser	Tyr	Ile	Lys	Lys	Lys	Glu	Cys	Tyr	Pro	Cys	Ser	His

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

965 970 975

Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp  
980 985 990

Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
995 1000 1005

Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu  
1010 1015 1020

Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn  
1025 1030 1035

Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu  
1040 1045 1050

Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg  
1055 1060 1065

Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly  
1070 1075 1080

Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn  
1085 1090 1095

His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro  
1100 1105 1110

Asn Phe Gln Ser Tyr Asp Leu Asp Thr  
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<213> Artificial Sequence

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<400> 295

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<210> 296

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 296

cctaaactga actggacca 19

<210> 297

<211> 19

<212> DNA

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<223> Synthetic Oligonucleotide Probe

<400> 297

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
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<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 298

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<210> 299

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 299

cattcccagt ataaaaattt tc 22

<210> 300

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 300

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<210> 301

<211> 24

<212> DNA

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<220>

<223> Synthetic Oligonucleotide Probe

<400> 301

gtgcctctcg gttaccacca atgg 24

<210> 302

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 302

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<210> 303

<211> 28

<212> DNA

<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>

<223> Synthetic oligonucleotide Probe

<400> 303

gcctttgaca accttcagtc actagtgg 28

<210> 304

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide Probe

<400> 304

ccccatgtgt ccatgactgt tccc 24

<210> 305

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide Probe

<400> 305

tactgcctca tgacctcttc actcccttgc atcatcttag agcgg 45

<210> 306

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide Probe

<400> 306

actccaagga aatcgatcc gttc 24

<210> 307

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 307

ttagcagctg aggatgggca caac 24

<210> 308

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide Probe

<400> 308

actccaagga aatcgatcc gttc 24

<210> 309

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 309

gccttcactg gtttggatgc attggagcat ctagacctga gtgacaacgc 50

<210> 310

<211> 3296

<212> DNA

<213> Homo Sapien

<400> 310

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gcgccgctcg gcgccggggc gcagcaggga aggggaagct gtggtctgcc 150  
ctgctccacg aggcgccact ggtgtgaacc gggagagccc ctgggtgggtc 200  
ccgtccccta tccctccttt atatagaaac cttccacact gggaaggcag 250  
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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<223> Synthetic Oligonucleotide Probe

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<210> 313

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<212> DNA

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<223> Synthetic Oligonucleotide Probe

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<210> 314

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<212> DNA

<213> Homo Sapien

<400> 314

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
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gcacagagag ggtggcgacc agctgttctc catatgcact aagaatagaa 1900

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<210> 315

<211> 509

<212> PRT

<213> Homo Sapien

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys
 35          40          45
Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys
 50          55          60
Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys
 65          70          75
Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu
 80          85          90
Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met
 95          100          105
Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met
110          115          120
Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met
125          130          135
Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg
140          145          150
Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg
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Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys
170          175          180
Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys
185          190          195
Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr
200          205          210
Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys
215          220          225
Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys
230          235          240
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245          250          255
Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro
260          265          270
Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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Ala Ser Thr Pro	Pro Gly Gly Ile Thr	Val Asp Asn Arg Val	Gln
	365	370	375
Thr Asp Pro Gln	Lys Pro Arg Gly Asp	Val Phe Ser Val Leu	Val
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His Ser Cys Asn	Phe Asp His Gly Leu	Cys Gly Trp Ile Arg	Glu
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Lys Asp Asn Asp	Leu His Trp Glu Pro	Ile Arg Asp Pro Ala	Gly
	410	415	420
Gly Gln Tyr Leu	Thr Val Ser Ala Ala	Lys Ala Pro Gly Gly	Lys
	425	430	435
Ala Ala Arg Leu	Val Leu Pro Leu Gly	Arg Leu Met His Ser	Gly
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Asp Leu Cys Leu	Ser Phe Arg His Lys	Val Thr Gly Leu His	Ser
	455	460	465
Gly Thr Leu Gln	Val Phe Val Arg Lys	His Gly Ala His Gly	Ala
	470	475	480
Ala Leu Trp Gly	Arg Asn Gly Gly His	Gly Trp Arg Gln Thr	Gln
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<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 316

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<210> 317

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 317

ttgcacttgt aggaccacg tacg 24

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 318  
 <211> 50  
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 <213> Homo Sapien

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 cactccagca tcagacatcc agatcatatg gctatttgag agaccccaca 250  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 ggattccaag caggtctgtt ccagcctctg attgtgtatc ggggcaagat 1350  
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<210> 320  
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 Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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Ser Ala Ser Gln	Lys 125	Ile Gln Val Thr	Val 130	Asp Asp Pro Val	Thr 135
Lys Pro Val Val	Gln 140	Ile His Pro Pro	Ser 145	Gly Ala Val Glu	Tyr 150
Val Gly Asn Met	Thr 155	Leu Thr Cys His	Val 160	Glu Gly Gly Thr	Arg 165
Leu Ala Tyr Gln	Trp 170	Leu Lys Asn Gly	Arg 175	Pro Val His Thr	Ser 180
Ser Thr Tyr Ser	Phe 185	Ser Pro Gln Asn	Asn 190	Thr Leu His Ile	Ala 195
Pro Val Thr Lys	Glu 200	Asp Ile Gly Asn	Tyr 205	Ser Cys Leu Val	Arg 210
Asn Pro Val Ser	Glu 215	Met Glu Ser Asp	Ile 220	Ile Met Pro Ile	Ile 225
Tyr Tyr Gly Pro	Tyr 230	Gly Leu Gln Val	Asn 235	Ser Asp Lys Gly	Leu 240
Lys Val Gly Glu	Val 245	Phe Thr Val Asp	Leu 250	Gly Glu Ala Ile	Leu 255
Phe Asp Cys Ser	Ala 260	Asp Ser His Pro	Pro 265	Asn Thr Tyr Ser	Trp 270
Ile Arg Arg Thr	Asp 275	Asn Thr Thr Tyr	Ile 280	Ile Lys His Gly	Pro 285
Arg Leu Glu Val	Ala 290	Ser Glu Lys Val	Ala 295	Gln Lys Thr Met	Asp 300
Tyr Val Cys Cys	Ala 305	Tyr Asn Asn Ile	Thr 310	Gly Arg Gln Asp	Glu 315
Thr His Phe Thr	Val 320	Ile Ile Thr Ser	Val 325	Gly Leu Glu Lys	Leu 330
Ala Gln Lys Gly	Lys 335	Ser Leu Ser Pro	Leu 340	Ala Ser Ile Thr	Gly 345
Ile Ser Leu Phe	Leu 350	Ile Ile Ser Met	Cys 355	Leu Leu Phe Leu	Trp 360
Lys Lys Tyr Gln	Pro 365	Tyr Lys Val Ile	Lys 370	Gln Lys Leu Glu	Gly 375
Arg Pro Glu Thr	Glu 380	Tyr Arg Lys Ala	Gln 385	Thr Phe Ser Gly	His 390
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
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<210> 321  
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<220>  
<223> Synthetic Oligonucleotide Probe

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<210> 322

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<220>  
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<400> 322  
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<210> 323  
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<212> DNA  
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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

ataactgctc ttctactat ttatcattgt aaagatggtg aatttaggcg 350  
ctatcagggg ccaaggacta agaaggactt cataaacttt ataagtata 400  
aagagtggaa gagtattgag cccgtttcat catggtttgg tccaggttct 450  
gttctgatga gtagtatgtc agcactcttt cagctatcta tgtggatcag 500  
gacgtgccat aactacttta ttgaagacct tggattgcca gtgtggggat 550  
catatactgt ttttgcttta gcaactctgt tttccggact gttattagga 600  
ctctgtatga tatttgtggc agattgcctt tgtccttcaa aaaggcgag 650  
accacagcca taccataacc cttcaaaaaa attattatca gaatctgcac 700  
aacctttgaa aaaagtggag gaggaacaag aggcggatga agaagatgtt 750  
tcagaagaag aagctgaaag taaagaagga acaaacaag actttccaca 800  
gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850  
cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900  
aagattgatc attttgtttg gtttgaagtg aactgtgact tttttgaata 950  
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acataaaagc actaggtata caagtttgaa atatgattta agcacagtat 1050  
gatggtttta atagttctct aatttttgaa aaatcgtgcc aagcaataag 1100  
atztatgtat atttgtttta taataacctt tttcaagtct gagttttgaa 1150  
aatttacatt tcccaagtat tgcattattg aggtatttaa gaagattatt 1200  
ttagagaaaa atatttctca tttgatataa ttttctctg tttcactgtg 1250  
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agaaatgtgt atttcagtga caatttcgtg gtcttttttag aggtatattc 1350  
caaaatttcc ttgtattttt aggttatgca actaataaaa actaccttac 1400  
attaattaat tacagttttc tacacatggg aatacaggat atgctactga 1450  
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caaattggat gataatttct tggaacatt ttttatgttt tagtaaacag 1600  
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aacaatctgt tgtaatttaa aattttggcc acttttttca gattttacat 1700  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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aaataataac atttttatat tttttaaaag acaaacttca tattatcctg 2000  
tggtctttcc tgactggtaa tattgtgtgg gatttcacag gtaaaagtca 2050  
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tctgttgctg tgtgaatcca ttagatttac agtatcgtaa tatacaagtt 2250  
ttctttaaag ccctctcctt tagaatttaa aatattgtac cattaaagag 2300  
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<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

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				20					25					30	
Val	Arg	Val	Ile	Thr	Asp	Glu	Asn	Trp	Arg	Glu	Leu	Leu	Glu	Gly	
				35					40					45	
Asp	Trp	Met	Ile	Glu	Phe	Tyr	Ala	Pro	Trp	Cys	Pro	Ala	Cys	Gln	
				50					55					60	
Asn	Leu	Gln	Pro	Glu	Trp	Glu	Ser	Phe	Ala	Glu	Trp	Gly	Glu	Asp	
				65					70					75	
Leu	Glu	Val	Asn	Ile	Ala	Lys	Val	Asp	Val	Thr	Glu	Gln	Pro	Gly	
				80					85					90	
Leu	Ser	Gly	Arg	Phe	Ile	Ile	Thr	Ala	Leu	Pro	Thr	Ile	Tyr	His	
				95					100					105	
Cys	Lys	Asp	Gly	Glu	Phe	Arg	Arg	Tyr	Gln	Gly	Pro	Arg	Thr	Lys	
				110					115					120	
Lys	Asp	Phe	Ile	Asn	Phe	Ile	Ser	Asp	Lys	Glu	Trp	Lys	Ser	Ile	
				125					130					135	
Glu	Pro	Val	Ser	Ser	Trp	Phe	Gly	Pro	Gly	Ser	Val	Leu	Met	Ser	
				140					145					150	
Ser	Met	Ser	Ala	Leu	Phe	Gln	Leu	Ser	Met	Trp	Ile	Arg	Thr	Cys	
				155					160					165	
His	Asn	Tyr	Phe	Ile	Glu	Asp	Leu	Gly	Leu	Pro	Val	Trp	Gly	Ser	
				170					175					180	

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu  
185 190 195  
Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys  
200 205 210  
Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu  
215 220 225  
Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu  
230 235 240  
Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu  
245 250 255  
Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser  
260 265 270  
Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser  
275 280

<210> 326

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 326

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<210> 327

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 327

tatgtggatc aggacgtgcc 20

<210> 328

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 328

tgcagggttc agtctagatt g 21

<210> 329

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 329

ttgaaggaca aaggcaatct gccac 25

<210> 330

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 330

ggagtcttgc agttccccctg gcagtcctgg tgctgttgct ttggg 45

<210> 331

<211> 2168

<212> DNA

<213> Homo Sapien

<400> 331

gcgagtgtcc agctgcggag acccgtgata attcggtaac taattcaaca 50  
aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taaccagtg 100  
ggacaggcgg attggaagag cgggaaggct ctggcccaga gcagtgtgac 150  
acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200  
ggtttggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250  
cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300  
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ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400  
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gagataggag ctgccaagac cctgatgaga cttcaggaca catacaggct 600  
ggacccaggc acaatttcca gaggggaact tccaggaacc aagtaccagg 650  
caatgctgag tgtggatgac tgctttggga tgggccgctc ggcctacaat 700  
gaaggggact attatcatac ggtgtttgtg atggagcagg tgctaaagca 750  
gcttgatgcc ggggaggagg ccaccacaac caagtcacag gtgctggact 800  
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ctcaccgcc gcctgtctc ccttgaccca agccacgaac gagctggagg 900  
gaatctgcgg tactttgagc agttattgga ggaagagaga gaaaaaacgt 950  
taacaaatca gacagaagct gagctagcaa cccagaagg catctatgag 1000  
aggcctgtgg actacctgcc tgagagggat gtttacgaga gcctctgtcg 1050

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 gaggaggacg agtgggacag cccgcacatc gtcagggtact acgatgtcat 1200  
 gtctgatgag gaaatcgaga ggatcaagga gatcgcaaaa cctaaacttg 1250  
 cacgagccac cgttcgtgat cccaagacag gagtcctcac tgtcgccagc 1300  
 taccgggttt ccaaaagctc ctggctagag gaagatgatg accctgttgt 1350  
 ggcccgagta aatcgtcgga tgcagcatat cacagggtta acagtaaaga 1400  
 ctgcagaatt gttacagggt gcaaattatg gagtgggagg acagtatgaa 1450  
 ccgcacttcg acttctctag gcgacctttt gacagcggcc tcaaaacaga 1500  
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 tcaacagaag ttgactgaca tccttttctg tccttcccct tcctggtcct 1800  
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 accatactag ggcgactcct gtgtgactga agtcccagcc cttccattca 1950  
 gcctgtgcc a tccctggccc caaggctagg atcaaagtgg ctgcagcaga 2000  
 gttagctgtc tagcgcctag caagggtcct ttgtacctca ggtgttttag 2050  
 gtgtgagatg tttcagtga ccaaagttct gataccttgt ttacatgttt 2100  
 gtttttatgg catttctatc tattgtggct ttacaaaaa ataaaatgtc 2150  
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<210> 332  
 <211> 533  
 <212> PRT  
 <213> Homo Sapien

<400> 332  
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 Leu Ser Cys Val Gln Ala Glu Phe Phe Thr Ser Ile Gly His Met  
 20 25 30  
 Thr Asp Leu Ile Tyr Ala Glu Lys Glu Leu Val Gln Ser Leu Lys  
 35 40 45  
 Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser  
 50 55 60

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp	65	70	75
Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val	80	85	90
Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu	95	100	105
Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg	110	115	120
Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala	125	130	135
Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile	140	145	150
Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser	155	160	165
Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly	170	175	180
Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln	185	190	195
Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Thr	Lys	Ser	Gln	Val	Leu	200	205	210
Asp	Tyr	Leu	Ser	Tyr	Ala	Val	Phe	Gln	Leu	Gly	Asp	Leu	His	Arg	215	220	225
Ala	Leu	Glu	Leu	Thr	Arg	Arg	Leu	Leu	Ser	Leu	Asp	Pro	Ser	His	230	235	240
Glu	Arg	Ala	Gly	Gly	Asn	Leu	Arg	Tyr	Phe	Glu	Gln	Leu	Leu	Glu	245	250	255
Glu	Glu	Arg	Glu	Lys	Thr	Leu	Thr	Asn	Gln	Thr	Glu	Ala	Glu	Leu	260	265	270
Ala	Thr	Pro	Glu	Gly	Ile	Tyr	Glu	Arg	Pro	Val	Asp	Tyr	Leu	Pro	275	280	285
Glu	Arg	Asp	Val	Tyr	Glu	Ser	Leu	Cys	Arg	Gly	Glu	Gly	Val	Lys	290	295	300
Leu	Thr	Pro	Arg	Arg	Gln	Lys	Arg	Leu	Phe	Cys	Arg	Tyr	His	His	305	310	315
Gly	Asn	Arg	Ala	Pro	Gln	Leu	Leu	Ile	Ala	Pro	Phe	Lys	Glu	Glu	320	325	330
Asp	Glu	Trp	Asp	Ser	Pro	His	Ile	Val	Arg	Tyr	Tyr	Asp	Val	Met	335	340	345
Ser	Asp	Glu	Glu	Ile	Glu	Arg	Ile	Lys	Glu	Ile	Ala	Lys	Pro	Lys	350	355	360
Leu	Ala	Arg	Ala	Thr	Val	Arg	Asp	Pro	Lys	Thr	Gly	Val	Leu	Thr	365	370	375



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Val	Ala	Ser	Tyr	Arg	Val	Ser	Lys	Ser	Ser	Trp	Leu	Glu	Glu	Asp
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Asp	Asp	Pro	Val	Val	Ala	Arg	Val	Asn	Arg	Arg	Met	Gln	His	Ile
				395					400					405
Thr	Gly	Leu	Thr	Val	Lys	Thr	Ala	Glu	Leu	Leu	Gln	Val	Ala	Asn
				410					415					420
Tyr	Gly	Val	Gly	Gly	Gln	Tyr	Glu	Pro	His	Phe	Asp	Phe	Ser	Arg
				425					430					435
Arg	Pro	Phe	Asp	Ser	Gly	Leu	Lys	Thr	Glu	Gly	Asn	Arg	Leu	Ala
				440					445					450
Thr	Phe	Leu	Asn	Tyr	Met	Ser	Asp	Val	Glu	Ala	Gly	Gly	Ala	Thr
				455					460					465
Val	Phe	Pro	Asp	Leu	Gly	Ala	Ala	Ile	Trp	Pro	Lys	Lys	Gly	Thr
				470					475					480
Ala	Val	Phe	Trp	Tyr	Asn	Leu	Leu	Arg	Ser	Gly	Glu	Gly	Asp	Tyr
				485					490					495
Arg	Thr	Arg	His	Ala	Ala	Cys	Pro	Val	Leu	Val	Gly	Cys	Lys	Trp
				500					505					510
Val	Ser	Asn	Lys	Trp	Phe	His	Glu	Arg	Gly	Gln	Glu	Phe	Leu	Arg
				515					520					525
Pro	Cys	Gly	Ser	Thr	Glu	Val	Asp							
				530										

<210> 333  
 <211> 18  
 <212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 333  
 ccaggcacaa tttccaga 18

<210> 334  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 334  
 ggacccttct gtgtgccag 19

<210> 335  
 <211> 19  
 <212> DNA  
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<220>  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 335  
 ggtctcaaga actcctgtc 19

<210> 336  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 336  
 acactcagca ttgcctggta cttg 24

<210> 337  
 <211> 45  
 <212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

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<210> 338  
 <211> 2789

<212> DNA  
 <213> Homo Sapien

<400> 338  
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 agacaggaca atcttcttgg ggatgctggc cctggaagcc agcgggcctt 200  
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 tcgagagctc ggctagacca aagtgatgaa gacttcaaac cccggattgt 550  
 cccctactac agggacccca acaagcccta caagaagggtg ctcaggactc 600  
 ggtacatcca gacagagctg ggctcccgtg agcggttgct ggtggctgtc 650  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 agctggtgct gccactcctg gtggctgaag ctgctgcagc cccggctttc 1850  
 ctcgaggcgt ttgcagccaa tgtcctggag ccacgagaac atgcattgct 1900  
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 acccatttct tggggtgaag gctgcagcag cggagttaga gcgacggtac 2000  
 cctgggacga ggctggcctg gctcgtctg cgagcagagg ccccttcca 2050  
 ggtgcgactc atggacgtgg tctcgaagaa gcaccctgtg gacactctct 2100  
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 ccaggagttc aatcctgccc tgtcaccaca gagatcacc ccaggggccc 2250  
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 ggggctccta taggggggag atttgaccgg caggcttctg cggagggtg 2350

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

cttctacaac gctgactacc tggcggcccg agcccggctg gcaggtgaac 2400  
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 gttttctctc ggttctcagg gctccacctc tttcgggccg tagagccagg 2500  
 gctggtgcag aagttctccc tgcgagactg cagcccacgg ctgagtgaag 2550  
 aactctacca ccgctgccgc ctcagcaacc tggaggggct agggggccgt 2600  
 gcccagctgg ctatggctct ctttgagcag gagcaggcca atagcactta 2650  
 gccgcctgg gggccctaac ctcattacct ttcctttgtc tgcctcagcc 2700  
 ccaggaaggg caaggcaaga tggtagacag atagagaatt gttgctgtat 2750  
 tttttaata tgaaaatgtt attaaacatg tcttctgcc 2789

<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

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Leu	Ile	Leu	Gly	Leu	Ser	Leu	Gly	Cys	Ser	Leu	Ser	Leu	Leu	Arg
			20						25					30
Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala
			35						40					45
Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg
			50						55					60
Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr
			65						70					75
Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg
			80						85					90
Tyr	Ile	Gln	Thr	Glu	Leu	Gly	Ser	Arg	Glu	Arg	Leu	Leu	Val	Ala
			95						100					105
Val	Leu	Thr	Ser	Arg	Ala	Thr	Leu	Ser	Thr	Leu	Ala	Val	Ala	Val
			110						115					120
Asn	Arg	Thr	Val	Ala	His	His	Phe	Pro	Arg	Leu	Leu	Tyr	Phe	Thr
			125						130					135
Gly	Gln	Arg	Gly	Ala	Arg	Ala	Pro	Ala	Gly	Met	Gln	Val	Val	Ser
			140						145					150
His	Gly	Asp	Glu	Arg	Pro	Ala	Trp	Leu	Met	Ser	Glu	Thr	Leu	Arg
			155						160					165
His	Leu	His	Thr	His	Phe	Gly	Ala	Asp	Tyr	Asp	Trp	Phe	Phe	Ile
			170						175					180
Met	Gln	Asp	Asp	Thr	Tyr	Val	Gln	Ala	Pro	Arg	Leu	Ala	Ala	Leu
			185						190					195

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ala Gly His Leu	Ser 200	Ile Asn Gln Asp	Leu 205	Tyr Leu Gly Arg	Ala 210
Glu Glu Phe Ile	Gly 215	Ala Gly Glu Gln	Ala 220	Arg Tyr Cys His	Gly 225
Gly Phe Gly Tyr	Leu 230	Leu Ser Arg Ser	Leu 235	Leu Leu Arg Leu	Arg 240
Pro His Leu Asp	Gly 245	Cys Arg Gly Asp	Ile 250	Leu Ser Ala Arg	Pro 255
Asp Glu Trp Leu	Gly 260	Arg Cys Leu Ile	Asp 265	Ser Leu Gly Val	Gly 270
Cys Val Ser Gln	His 275	Gln Gly Gln Gln	Tyr 280	Arg Ser Phe Glu	Leu 285
Ala Lys Asn Arg	Asp 290	Pro Glu Lys Glu	Gly 295	Ser Ser Ala Phe	Leu 300
Ser Ala Phe Ala	Val 305	His Pro Val Ser	Glu 310	Gly Thr Leu Met	Tyr 315
Arg Leu His Lys	Arg 320	Phe Ser Ala Leu	Glu 325	Leu Glu Arg Ala	Tyr 330
Ser Glu Ile Glu	Gln 335	Leu Gln Ala Gln	Ile 340	Arg Asn Leu Thr	Val 345
Leu Thr Pro Glu	Gly 350	Glu Ala Gly Leu	Ser 355	Trp Pro Val Gly	Leu 360
Pro Ala Pro Phe	Thr 365	Pro His Ser Arg	Phe 370	Glu Val Leu Gly	Trp 375
Asp Tyr Phe Thr	Glu 380	Gln His Thr Phe	Ser 385	Cys Ala Asp Gly	Ala 390
Pro Lys Cys Pro	Leu 395	Gln Gly Ala Ser	Arg 400	Ala Asp Val Gly	Asp 405
Ala Leu Glu Thr	Ala 410	Leu Glu Gln Leu	Asn 415	Arg Arg Tyr Gln	Pro 420
Arg Leu Arg Phe	Gln 425	Lys Gln Arg Leu	Leu 430	Asn Gly Tyr Arg	Arg 435
Phe Asp Pro Ala	Arg 440	Gly Met Glu Tyr	Thr 445	Leu Asp Leu Leu	Leu 450
Glu Cys Val Thr	Gln 455	Arg Gly His Arg	Arg 460	Ala Leu Ala Arg	Arg 465
Val Ser Leu Leu	Arg 470	Pro Leu Ser Arg	Val 475	Glu Ile Leu Pro	Met 480
Pro Tyr Val Thr	Glu 485	Ala Thr Arg Val	Gln 490	Leu Val Leu Pro	Leu 495
Leu Val Ala Glu	Ala 500	Ala Ala Ala Pro	Ala 505	Phe Leu Glu Ala	Phe 510

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ala Ala Asn Val	Leu	Glu	Pro	Arg	Glu	His	Ala	Leu	Leu	Thr	Leu
	515					520					525
Leu Leu Val Tyr	Gly	Pro	Arg	Glu	Gly	Gly	Arg	Gly	Ala	Pro	Asp
	530					535					540
Pro Phe Leu Gly	Val	Lys	Ala	Ala	Ala	Ala	Glu	Leu	Glu	Arg	Arg
	545					550					555
Tyr Pro Gly Thr	Arg	Leu	Ala	Trp	Leu	Ala	Val	Arg	Ala	Glu	Ala
	560					565					570
Pro Ser Gln Val	Arg	Leu	Met	Asp	Val	Val	Ser	Lys	Lys	His	Pro
	575					580					585
Val Asp Thr Leu	Phe	Phe	Leu	Thr	Thr	Val	Trp	Thr	Arg	Pro	Gly
	590					595					600
Pro Glu Val Leu	Asn	Arg	Cys	Arg	Met	Asn	Ala	Ile	Ser	Gly	Trp
	605					610					615
Gln Ala Phe Phe	Pro	Val	His	Phe	Gln	Glu	Phe	Asn	Pro	Ala	Leu
	620					625					630
Ser Pro Gln Arg	Ser	Pro	Pro	Gly	Pro	Pro	Gly	Ala	Gly	Pro	Asp
	635					640					645
Pro Pro Ser Pro	Pro	Gly	Ala	Asp	Pro	Ser	Arg	Gly	Ala	Pro	Ile
	650					655					660
Gly Gly Arg Phe	Asp	Arg	Gln	Ala	Ser	Ala	Glu	Gly	Cys	Phe	Tyr
	665					670					675
Asn Ala Asp Tyr	Leu	Ala	Ala	Arg	Ala	Arg	Leu	Ala	Gly	Glu	Leu
	680					685					690
Ala Gly Gln Glu	Glu	Glu	Glu	Ala	Leu	Glu	Gly	Leu	Glu	Val	Met
	695					700					705
Asp Val Phe Leu	Arg	Phe	Ser	Gly	Leu	His	Leu	Phe	Arg	Ala	Val
	710					715					720
Glu Pro Gly Leu	Val	Gln	Lys	Phe	Ser	Leu	Arg	Asp	Cys	Ser	Pro
	725					730					735
Arg Leu Ser Glu	Glu	Leu	Tyr	His	Arg	Cys	Arg	Leu	Ser	Asn	Leu
	740					745					750
Glu Gly Leu Gly	Gly	Arg	Ala	Gln	Leu	Ala	Met	Ala	Leu	Phe	Glu
	755					760					765
Gln Glu Gln Ala	Asn	Ser	Thr								
	770										

<210> 340

<211> 1572

<212> DNA

<213> Homo Sapien

<400> 340

cgagtggtg cgccaacgtg agaggaaacc cgtgcgcggc tgcgctttcc 50

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

tgcccccaag ccgttctaga cgcgggaaaa atgctttctg aaagcagctc 100  
ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150  
tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200  
catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250  
ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300  
ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350  
accaaact gtgacaaagc agagtcttc agttctgaaa atgttaaagt 400  
gtttgagtca attaatatgg acacaaatga catgtggtta atgatgagaa 450  
aagcttaca atacgccttt gataagtata gagaccaata caactgggtc 500  
ttccttgac gccccactac gtttgctatc attgaaaacc taaagtattt 550  
tttgtaaaa aaggatccat cacagccttt ctatctaggc cacactataa 600  
aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650  
gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagt 700  
tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750  
cagtttgcct gaaatatgct ggagtatttg cagaaaatgc agaagatgct 800  
gatggaaaag atgtatttaa taccaaatct gttgggcttt ctattaaaga 850  
ggcaatgact tatcaccca accaggtagt agaaggctgt tgttcagata 900  
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tatggggat accgccttag ggcatttggg catattttca atgatgcatt 1000  
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gtaactacat atccaatata gctgtatgtt tctttttctt ttctaatttg 1150  
gtggcactgg tataaccaca cattaaagtc agtagtacat ttttaaata 1200  
gggtgggttt tttctttaaa acacatgaac attgtaaatg tgttggaaag 1250  
aagtgtttta agaataataa ttttgcaaat aaactattaa taaatattat 1300  
atgtgataaa ttctaaatta tgaacattag aaatctgtgg ggcacatatt 1350  
tttctgatt gggtaaaaaa ttttaacagg tcttttagcgt tctaagatat 1400  
gcaaatgata tctctagtgt tgaatttgtg attaaagtaa aacttttagc 1450  
tgtgtgttcc ctttacttct aatactgatt tatgttctaa gcctcccaa 1500  
gttccaatgg atttgccttc tcaaaatgta caactaagca actaaagaaa 1550  
attaaagtga aagttgaaaa at 1572

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 341

Met Leu Ser Glu Ser Ser Ser Phe Leu Lys Gly Val Met Leu Gly  
1 5 10 15Ser Ile Phe Cys Ala Leu Ile Thr Met Leu Gly His Ile Arg Ile  
20 25 30Gly His Gly Asn Arg Met His His His Glu His His His Leu Gln  
35 40 45Ala Pro Asn Lys Glu Asp Ile Leu Lys Ile Ser Glu Asp Glu Arg  
50 55 60Met Glu Leu Ser Lys Ser Phe Arg Val Tyr Cys Ile Ile Leu Val  
65 70 75Lys Pro Lys Asp Val Ser Leu Trp Ala Ala Val Lys Glu Thr Trp  
80 85 90Thr Lys His Cys Asp Lys Ala Glu Phe Phe Ser Ser Glu Asn Val  
95 100 105Lys Val Phe Glu Ser Ile Asn Met Asp Thr Asn Asp Met Trp Leu  
110 115 120Met Met Arg Lys Ala Tyr Lys Tyr Ala Phe Asp Lys Tyr Arg Asp  
125 130 135Gln Tyr Asn Trp Phe Phe Leu Ala Arg Pro Thr Thr Phe Ala Ile  
140 145 150Ile Glu Asn Leu Lys Tyr Phe Leu Leu Lys Lys Asp Pro Ser Gln  
155 160 165Pro Phe Tyr Leu Gly His Thr Ile Lys Ser Gly Asp Leu Glu Tyr  
170 175 180Val Gly Met Glu Gly Gly Ile Val Leu Ser Val Glu Ser Met Lys  
185 190 195Arg Leu Asn Ser Leu Leu Asn Ile Pro Glu Lys Cys Pro Glu Gln  
200 205 210Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala Val  
215 220 225Cys Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala  
230 235 240Asp Gly Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Ser Ile  
245 250 255Lys Glu Ala Met Thr Tyr His Pro Asn Gln Val Val Glu Gly Cys  
260 265 270Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln  
275 280 285

Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

290

295

300

His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser  
305 310 315

Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

tccccaagcc gttctagacg cgg 23

<210> 343

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 344

gcccaaagtc cctaaggcgg tatacccc 28

<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 345

gggtgtgatg cttggaagca ttttctgtgc tttgatcact atgctaggac 50

<210> 346

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 346

gggatgcagg tgggtgtctca tgggg 25

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 347  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 347  
ccctcatgta ccggctcc 18  
  
<210> 348  
<211> 48  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 348  
ggattctaatt acgactcact atagggctca gaaaagcgca acagagaa 48  
  
<210> 349  
<211> 47  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 349  
ctatgaaatt aaccctcact aaagggatgt cttccatgcc aaccttc 47  
  
<210> 350  
<211> 48  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 350  
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<211> 48  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 351  
ctatgaaatt aaccctcact aaagggacga ggaagatggg cggatggt 48  
  
<210> 352  
<211> 47  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 352  
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<210> 353  
 <211> 48  
 <212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 353  
 ctatgaaattaacccctcactaaagggacggggacaccacggaccaga 48

<210> 354  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 354  
 ggattctaatacgcactcactatagggcttgctgcggtttttgttcctg 48

<210> 355  
 <211> 48  
 <212> DNA  
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<220>  
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<400> 355  
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<210> 356  
 <211> 46  
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<400> 356  
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<210> 357  
 <211> 48  
 <212> DNA  
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<220>  
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<400> 357  
 ctatgaaattaacccctcactaaagggagcccgggcatggtctcagtta 48

<210> 358  
 <211> 47  
 <212> DNA  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>

<223> Synthetic Oligonucleotide Probe

<400> 358

ggattctaatacgcactcactatagggcggaagatggcga ggaggag 47

<210> 359

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 359

ctatgaaatt aaccctcact aaagggacca aggccacaaa cggaaatc 48

<210> 360

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 360

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<210> 361

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 361

ctatgaaatt aaccctcact aaaggggagg tacaattaag gggtaggat 48

<210> 362

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 362

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<210> 363

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 363

ctatgaaatt aaccctcact aaaggggagga ttgccgcgac cctcacag 48

<210> 364

<211> 47

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 364  
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<210> 365  
 <211> 48  
 <212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 365  
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<210> 366  
 <211> 48  
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 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 366  
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<210> 367  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 367  
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<210> 368  
 <211> 47  
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 <213> Artificial Sequence

<220>  
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<400> 368  
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<210> 369  
 <211> 48  
 <212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 369

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
ctatgaaatt aaccctcact aaagggaaag acatgtcatc gggagtgg 48

<210> 370

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 370

ggattctaatt acgactcact atagggccgg gtggaggtgg aacagaaa 48

<210> 371

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 371

ctatgaaatt aaccctcact aaagggacac agacagagcc ccatacgc 48

<210> 372

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 372

ggattctaatt acgactcact atagggccag ggaaatccgg atgtctc 47

<210> 373

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 373

ctatgaaatt aaccctcact aaagggagta aggggatgcc accgagta 48

<210> 374

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 374

ggattctaatt acgactcact atagggccag ctacccgcag gaggagg 47

<210> 375

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 375

ctatgaaatt aaccctcact aaagggatcc caggtgatga ggtccaga 48

<210> 376

<211> 997

<212> DNA

<213> Homo Sapien

<400> 376

cccacgcgtc cgatcttacc aacaaaacac tcctgaggag aaagaaagag 50  
 agggaggaggag agaaaaagag agagagagaa acaaaaaacc aaagagagag 100  
 aaaaaatgaa ttcatctaaa tcatctgaaa cacaatgcac agagagagga 150  
 tgcttctctt cccaaatgtt cttatggact gttgctggga tccccatcct 200  
 atttctcagt gcctgtttca tcaccagatg tgttgtagaca tttcgcatct 250  
 ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300  
 ctctcctgct acaattatgg atcagggttca gtcaagaatt gttgtccatt 350  
 gaactgggaa tatTTTTcaat ccagctgcta cttcttttct actgacacca 400  
 tttcctgggc gttaagttta aagaactgct cagccatggg ggctcacctg 450  
 gtgggttatca actcacagga ggagcaggaa ttccttttct acaagaaacc 500  
 taaaatgaga gagtttttta ttggactgtc agaccagggt gtcgaggggtc 550  
 agtggcaatg ggtggacggc acacctttga caaagtctct gagcttctgg 600  
 gatgtagggg agcccaacaa catagctacc ctggaggact gtgccaccat 650  
 gagagactct tcaaacccaa ggcaaaattg gaatgatgta acctgtttcc 700  
 tcaattattt tcggatttgt gaaatggtag gaataaatcc tttgaacaaa 750  
 ggaaaatctc ttttaagaaca gaaggcaca ctcaaattgtg taaagaagga 800  
 agagcaagaa catggccaca cccaccgccc cacacgagaa atttgtgcgc 850  
 tgaacttcaa aggacttcat aagtatttgt tactctgata caaataaaaa 900  
 taagtagttt taaatgttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 950  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 997

<210> 377

<211> 219

<212> PRT

<213> Homo Sapien

<400> 377

Met Asn Ser Ser Lys Ser Ser Glu Thr Gln Cys Thr Glu Arg Gly  
 1 5 10 15

Cys Phe Ser Ser Gln Met Phe Leu Trp Thr Val Ala Gly Ile Pro  
 20 25 30

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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Ile Leu Phe Leu Ser Ala Cys Phe Ile Thr Arg Cys Val Val Thr
      35                                40                                45

Phe Arg Ile Phe Gln Thr Cys Asp Glu Lys Lys Phe Gln Leu Pro
      50                                55                                60

Glu Asn Phe Thr Glu Leu Ser Cys Tyr Asn Tyr Gly Ser Gly Ser
      65                                70                                75

Val Lys Asn Cys Cys Pro Leu Asn Trp Glu Tyr Phe Gln Ser Ser
      80                                85                                90

Cys Tyr Phe Phe Ser Thr Asp Thr Ile Ser Trp Ala Leu Ser Leu
      95                                100                               105

Lys Asn Cys Ser Ala Met Gly Ala His Leu Val Val Ile Asn Ser
     110                               115                               120

Gln Glu Glu Gln Glu Phe Leu Ser Tyr Lys Lys Pro Lys Met Arg
     125                               130                               135

Glu Phe Phe Ile Gly Leu Ser Asp Gln Val Val Glu Gly Gln Trp
     140                               145                               150

Gln Trp Val Asp Gly Thr Pro Leu Thr Lys Ser Leu Ser Phe Trp
     155                               160                               165

Asp Val Gly Glu Pro Asn Asn Ile Ala Thr Leu Glu Asp Cys Ala
     170                               175                               180

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val
     185                               190                               195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile
     200                               205                               210

Asn Pro Leu Asn Lys Gly Lys Ser Leu
     215

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<210> 378

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 378

ttcagcttct gggatgtagg g 21

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 379

tattcctacc atttcacaaa tccg 24

<210> 380

<211> 49



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

ggaggactgt gccaccatga gagactcttc aaaccaagg caaaattgg 49

<210> 381

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 381

gcagattttg aggacagcca cctcca 26

<210> 382

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 382

ggccttgag acaaccgt 18

<210> 383

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 383

cagactgagg gagatccgag a 21

<210> 384

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 384

cagctgccct tccccaacca 20

<210> 385

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 385

catcaagcgc ctctacca 18

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 386  
<211> 21  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 386  
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<210> 388  
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<400> 388  
gggatgtggt gaacacagaa ca 22

<210> 389  
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<210> 390  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<223> Synthetic oligonucleotide probe

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<210> 396

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<210> 398
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

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<210> 399
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<400> 399
ccaggagagc tggcgatg 18

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<210> 401
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<400> 401
cacagagcat ttgtccatca gcagttcag 29

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<400> 404  
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<210> 405  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<400> 410  
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<210> 412  
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<212> DNA  
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<210> 413  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>  
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<400> 418  
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<210> 419  
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<212> DNA  
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<220>  
<223> synthetic oligonucleotide probe

<400> 419  
gggccctaac ctcattacct tt 22

<210> 420

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 23  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 420  
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<210> 421  
<211> 21  
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<220>  
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<400> 421  
tctgtccacc atcttgccctt g 21

<210> 422  
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tcaaattccag caatcgaacc ccagtggtag aggaatttga aagtgtggaa 200  
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gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300  
ttcagggaga cttggcgggt cgtgcagaaa tactggggaa gacatccctg 350  
aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt 400  
cgttgctcga aatgaccgca aggaaattga tgagattgtg atcgagttaa 450  
ctgtgcaagt gaagccagtg acccctgtct gtagagtgcc gaaggctgta 500  
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agatggaagt ctatgacctg aacattggcg gaattattgg gggggttctg 800  
gttgctcctg ctgtactggc cctgatcacg ttgggcatct gctgtgcata 850  
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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

accagggaa accagatgga gttactaca tccgactga cgaggagggc 950  
gacttcagac acaagtcac gtttgtgatc tgagacccgc ggtgtggctg 1000  
agagcgaca gagcgacgt gcacatacct ctgctagaaa ctctgtcaa 1050  
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ttttcgtttt ggccaaagtt gaccactact cttcttactc taacaagcca 1150  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 cccactgttc ctctttgccca cagagaaagc acccagacgc cacaggctct 2600  
 gtcgcatttc aaaacaaacc atgatggagt ggcggccagt ccagcctttt 2650  
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 aagatatgaa tgtgactcaa gactcgaggc cgatacgagg ctgtgattct 3450  
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 20 25 30  
 Ala Val Asn Leu Lys Ser Ser Asn Arg Thr Pro Val Val Gln Glu  
 35 40 45  
 Phe Glu Ser Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr  
 50 55 60

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser	Asp	Pro	Arg	Ile	Glu	Trp	Lys	Lys	Ile	Gln	Asp	Glu	Gln	Thr	
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Thr	Tyr	Val	Phe	Phe	Asp	Asn	Lys	Ile	Gln	Gly	Asp	Leu	Ala	Gly	
				80					85					90	
Arg	Ala	Glu	Ile	Leu	Gly	Lys	Thr	Ser	Leu	Lys	Ile	Trp	Asn	Val	
				95					100					105	
Thr	Arg	Arg	Asp	Ser	Ala	Leu	Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg	
				110					115					120	
Asn	Asp	Arg	Lys	Glu	Ile	Asp	Glu	Ile	Val	Ile	Glu	Leu	Thr	Val	
				125					130					135	
Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val	
				140					145					150	
Pro	Val	Gly	Lys	Met	Ala	Thr	Leu	His	Cys	Gln	Glu	Ser	Glu	Gly	
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His	Pro	Arg	Pro	His	Tyr	Ser	Trp	Tyr	Arg	Asn	Asp	Val	Pro	Leu	
				170					175					180	
Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn	Ser	Ser	Phe	
				185					190					195	
His	Leu	Asn	Ser	Glu	Thr	Gly	Thr	Leu	Val	Phe	Thr	Ala	Val	His	
				200					205					210	
Lys	Asp	Asp	Ser	Gly	Gln	Tyr	Tyr	Cys	Ile	Ala	Ser	Asn	Asp	Ala	
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Gly	Ser	Ala	Arg	Cys	Glu	Glu	Gln	Glu	Met	Glu	Val	Tyr	Asp	Leu	
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Asn	Ile	Gly	Gly	Ile	Ile	Gly	Gly	Val	Leu	Val	Val	Leu	Ala	Val	
				245					250					255	
Leu	Ala	Leu	Ile	Thr	Leu	Gly	Ile	Cys	Cys	Ala	Tyr	Arg	Arg	Gly	
				260					265					270	
Tyr	Phe	Ile	Asn	Asn	Lys	Gln	Asp	Gly	Glu	Ser	Tyr	Lys	Asn	Pro	
				275					280					285	
Gly	Lys	Pro	Asp	Gly	Val	Asn	Tyr	Ile	Arg	Thr	Asp	Glu	Glu	Gly	
				290					295					300	
Asp	Phe	Arg	His	Lys	Ser	Ser	Phe	Val	Ile						
				305					310						